

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: December 5, 2004, 01:18:12 ; Search time 111 Seconds  
(without alignments)  
6550.784 Million cell updates/sec

Title: US-09-605-703B-1

Perfect score: 1023

Sequence: 1 aggcataaacacacagcagc.....tgcgggtttctatccggaat 1023

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.\*

- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	41.4	4.0	10095	3	US-08-822-586-45
C 2	41.4	4.0	4403765	3	US-09-103-840A-2
C 3	41.4	4.0	4411529	3	US-09-103-840A-1
C 4	40	3.9	1230	4	US-09-894-844-114
C 5	40	3.9	4403765	3	US-09-103-840A-2
C 6	40	3.9	4411529	3	US-09-103-840A-1
C 7	39.8	3.9	1119	4	US-09-252-991A-3537
C 8	39.8	3.9	1581	4	US-09-252-991A-3549
C 9	39.8	3.9	1947	4	US-09-252-991A-3557
C 10	39.2	3.8	465	4	US-09-252-991A-2233
C 11	39.2	3.8	852	4	US-09-252-991A-2447
C 12	39.2	3.8	1359	4	US-09-252-991A-2528
C 13	39.2	3.8	1473	4	US-09-252-991A-2391
C 14	38.4	3.8	876	4	US-09-252-991A-8411
C 15	38.4	3.8	1002	4	US-09-252-991A-8415
C 16	38.4	3.8	1074	4	US-09-252-991A-8465
C 17	38.2	3.7	1632	4	US-09-252-991A-1216
C 18	37.2	3.6	1674	4	US-09-252-991A-1253
C 19	36.8	3.6	924	4	US-09-252-991A-15733
C 20	36.8	3.6	1146	1	US-08-482-385A-1
C 21	36.8	3.6	1281	4	US-09-252-991A-15620
C 22	36.8	3.6	1623	4	US-09-252-991A-15700
C 23	36.8	3.6	2728	1	US-08-482-385A-5
C 24	36.8	3.6	9515	1	US-08-920-812-13
C 25	36.8	3.6	9515	1	US-08-920-827-13
C 26	36.8	3.6	9515	1	US-08-921-177-13
C 27	36.8	3.6	9515	1	US-08-362-577C-13

C 28	36.8	3.6	9515	2	US-08-920-828-13	Sequence 13, Appl
C 29	36.6	3.6	711	4	US-09-252-991A-14991	Sequence 14991, A
C 30	36.6	3.6	1314	4	US-09-489-039A-441	Sequence 441, App
C 31	36.6	3.6	1401	2	US-08-812-412-1	Sequence 1, Appl
C 32	36.6	3.6	1401	3	US-09-180-271-4	Sequence 4, Appl
C 33	36.6	3.6	1407	4	US-09-252-991A-14753	Sequence 14753, A
C 34	36.6	3.6	1428	4	US-09-252-991A-9266	Sequence 9266, Ap
C 35	36.6	3.6	1446	4	US-09-489-039A-634	Sequence 634, App
C 36	36.6	3.6	1545	4	US-09-252-991A-9274	Sequence 9274, Ap
C 37	36.6	3.6	1977	4	US-09-252-991A-9290	Sequence 9290, Ap
C 38	36.4	3.6	483	4	US-09-252-991A-10330	Sequence 10330, A
C 39	36.4	3.6	1746	4	US-09-252-991A-10643	Sequence 10643, A
C 40	36.4	3.6	2979	4	US-09-252-991A-10524	Sequence 10524, A
C 41	36	3.5	714	4	US-09-252-991A-11545	Sequence 11545, A
C 42	36	3.5	1023	4	US-09-252-991A-11604	Sequence 11604, A
C 43	36	3.5	1479	4	US-09-252-991A-11768	Sequence 11768, A
C 44	36	3.5	1968	4	US-09-252-991A-11840	Sequence 11840, A
C 45	36	3.5	28958	1	US-08-258-261B-6	Sequence 6, Appl

#### ALIGNMENTS

#### RESULT 1

US-08-822-586-45/c  
; Sequence 45, Application US/08822586  
; Patent No. 6015890  
; GENERAL INFORMATION:  
; APPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSER AND  
; APPLICANT: AMALIO TELENVI  
; TITLE OF INVENTION: AN EMBAR OPERON OF MYCOBACTERIA AND  
; TITLE OF INVENTION: MUTANTS THEREOF  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN  
; STREET: 90 PARK AVENUE  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: U.S.A.  
; ZIP: 10016  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE  
; MEDIUM TYPE: DISKETTE  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/822,586  
; FILING DATE: MARCH 20, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ELIZABETH A. BOGOSIAN  
; REGISTRATION NUMBER: 39,911  
; REFERENCE/DOCKET NUMBER: 96700/437  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 697-5995  
; TELEFAX: (212) 286-0854 or 286-0082  
; TELEX: TWX 710-581-4766  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10095  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: Genomic DNA  
; HYPOTHEetical: NO  
US-08-822-586-45

Query Match 4.0%; Score 41.4; DB 3; Length 10095;  
Best Local Similarity 55.1%; Pred. No. 0.077;  
Matches 81; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

663 GAAGCGACGACGTCGCGCTACCTGGAAGGCCCGACCGAATCTGCGATCCACGTGG 722

Db 8960 GACGCGACGAACACCGCGCCATGAAACCGGCACGATCGGTACCGGGGCTGTGTCGACG 8901  
QY 723 GCGTCGATCCGCTGCAGCGCGGAGCGCGCTGTTCCCGAAGAGCTGCGCGCGCTGA 782  
Db 8900 GCGCGGATCAGCGCGCTTCCGCGCGCGCGCGCGGCGGCGAAGTGCACGCGCGCATAG 8841  
QY 783 TCACCGGAGGATCCTTCGCTGAGGAAA 809  
Db 8840 CCGCGCGGATCGCAACACGCGGAAA 8814

## RESULT 2

US-09-103-840A-2/c  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4403765  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; OTHER INFORMATION: CDC 1551  
; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
; OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 4.0%; Score 41.4; DB 3; Length 4403765;  
Best Local Similarity 55.1%; Pred. No. 1.9; Mismatches 0; Gaps 0;  
Matches 81; Conservative 0;  
QY 663 GAACGCGACGACGTCGCGTACTGGAAGCGCCCGACCGCGAATCTGCGCATCCACGTGG 722  
Db 4240918 GACCGGACGACACCGCGCGCATGAAACCGCGCGCATCGTACCGGGGCTGTCAGC 4240859  
QY 723 GCGTCGATCCGCTGCAGCGCGGAGCGCGCGCTGTTGCCGAAGAGCTGCGCGCGCTGA 782  
Db 4240858 GCGCGGATCAGCGCGCTTCCGCGCGCGCGCGGCGGCGAAGTGCACGCGCGCATAG 4240799  
QY 783 TCACCGGAGGATCCTTCGCTGAGGAAA 809  
Db 4240798 CCGCGCGGATCGCAACACGCGGAAA 4240772

## RESULT 3

US-09-103-840A-1/c  
; Sequence 1, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4411529  
; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: H37RV  
US-09-103-840A-1  
Query Match 4.0%; Score 41.4; DB 3; Length 4411529;  
Best Local Similarity 55.1%; Pred. No. 1.9; Mismatches 0; Gaps 0;  
Matches 81; Conservative 0;  
QY 663 GAACGCGACGACGTCGCGTACTGGAAGCGCCCGACCGAATCTGCGCATCCACGTGG 722  
Db 4248672 GACCGGACGACACCGCGCGCATGAAACCGCGCGCATCGTACCGGGGCTGTCGTCAGC 4248613  
QY 723 GCGTCGATCCGCTGCAGCGCGGAGCGCGCGCTGTTGCCGAAGAGCTGCGCGCGCTGA 782  
Db 4248612 GCGCGGATCAGCGCGCTTCCGCGCGCGCGCGCGGCGGCGAAGTGCACGCGCGCATAG 4248553  
QY 783 TCACCGGAGGATCCTTCGCTGAGGAAA 809  
Db 4248552 CCGCGCGGATCGCAACACGCGGAAA 4248526

## RESULT 4

US-09-894-844-114  
; Sequence 114, Application US/09894844  
; Patent No. 6686166  
; GENERAL INFORMATION:  
; APPLICANT: Behr, Marcel  
; APPLICANT: Small, Peter  
; APPLICANT: Schoolnik, Gary  
; APPLICANT: Wilson, Michael A.  
; TITLE OF INVENTION: Molecular Differences Between Species of  
; FILE REFERENCE: STAN102CON  
; CURRENT APPLICATION NUMBER: US/09/894,844  
; CURRENT FILING DATE: 2001-06-27  
; PRIOR APPLICATION NUMBER: 09/318,191  
; PRIOR FILING DATE: 1999-05-25  
; PRIOR APPLICATION NUMBER: 60/097,936  
; PRIOR FILING DATE: 1998-08-25  
; NUMBER OF SEQ ID NOS: 137  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 114  
; LENGTH: 1230  
; TYPE: DNA  
; ORGANISM: Mycobacteria tuberculosis  
US-09-894-844-114

Query Match 3.9%; Score 40; DB 4; Length 1230;  
Best Local Similarity 49.5%; Pred. No. 0.067;  
Matches 103; Conservative 0; Mismatches 105; Indels 0; Gaps 0;  
QY 595 CCAACCCCGACCCCGTCTGTCGACCGAGGACCTGTTATTGAGGCGCATTTGTTT 654  
Db 567 CAACCAACTGCGAGCGCTGTGCCAACGCGCGCCAAAGCCACCGGGTGTGGCAACCG 626  
QY 655 TGAATGCGAAGCGAGCAAGTGCCTACTGGAAGGCCCGACCGAATCTGCGCAT 714  
Db 627 CACCGACGAGATCGTCCGCTTGTGCGCGACACCAATGTGTTGCGCAGCTGCGCAC 686  
QY 715 CCACGTGGCGTTCGATCCGCTGCACCGCGCGGACCGCGCTGTTGCCGAAGAGCTGCG 774  
Db 687 CCAAGCGCCCGCTTGGACCGGATCTGGCGCAACATCTCGGCGGTGGCCGAACACTGCG 746  
QY 775 CGCGCTGATCCCGAGGATCTTCGCTG 802  
Db 747 GGGCTTCATCGTGCAGAACCGCCAGCAG 774

## RESULT 5

US-09-103-840A-2  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:

APPLICANT: FLEISCHMAN, Robert D.  
APPLICANT: WHITE, Owen R.  
APPLICANT: FRASER, Claire M.  
APPLICANT: VENTER, John C.  
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
TITLE OF INVENTION: TUBERCULOSIS  
FILE REFERENCE: 24366-20007.00  
CURRENT APPLICATION NUMBER: US/09/103,840A  
CURRENT FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 4403765  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
FEATURE:  
OTHER INFORMATION: CDC 1551  
OTHER INFORMATION: "n" bases at various positions throughout the sequence  
OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 3.9%; Score 40; DB 3; Length 4403765;  
Best Local Similarity 49.5%; Pred. No. 4.9;  
Matches 103; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 595 CCAACCCAGCCACCGTCTGTCGACCGAGACCTGTTATTGAGCGCCATTGGTTT 654  
Db 2209490 CAACCACTGGCAGCCCTGCTGCGCAACGCGGCCAAGCCACCGGCTGGCCCAACCG 2209549

QY 655 TGAATGGAAGCAGCAGCACTGCTGCTGTAAGCGCCCGACCCGAAATCTGGCGAT 714  
Db 2209550 CACCGACAGATGTCGCGCTGGTGGCGACACGAATGTCTTGGCGAGCTGGCGAC 2209609

QY 715 CCAGTGGGCTGATCCGCTGACGCGCGCGAGCGCGCTGTTGCGGAAGAGTGGG 774  
Db 2209610 CCAAAGCCGCCCTTGGACCGGATCTGGCGGAACATCTCGCGGTGGCGCCGAACACTGCG 2209669

QY 775 CCGCTGATCAGCAGGATCTTCTGCTG 802  
Db 2209670 GGGCTTCATGCTGAGAACCGCCAGCAG 2209697

RESULT 6  
US-09-103-840A-1  
Sequence 1, Application US/09103840A  
Patent No. 6294328  
GENERAL INFORMATION:  
APPLICANT: FLEISCHMAN, Robert D.  
APPLICANT: WHITE, Owen R.  
APPLICANT: FRASER, Claire M.  
APPLICANT: VENTER, John C.  
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
TITLE OF INVENTION: TUBERCULOSIS  
FILE REFERENCE: 24366-20007.00  
CURRENT APPLICATION NUMBER: US/09/103,840A  
CURRENT FILING DATE: 1998-06-24  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 4411529  
TYPE: DNA  
ORGANISM: Mycobacterium tuberculosis  
OTHER INFORMATION: H37RV  
US-09-103-840A-1

Query Match 3.9%; Score 40; DB 3; Length 4411529;  
Best Local Similarity 49.5%; Pred. No. 4.9;  
Matches 103; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 595 CCAACCCAGCCACCGTCTGTCGACCGAGACCTGTTATTGAGCGCCATTGGTTT 654  
Db 2212190 CAACCACTGGCAGCCTGCTGCGCAACGCGGCCAAGCCACCGGCTGTGGCCACCG 2212249

QY 655 TGAATGGAAGCAGCAGCACTGCTGTAAGCGCCCGACCCGAAATCTGGCGAT 714  
Db 2212250 CACCGACAGATGTCGCGCTGGTGGCGACACGAATGTGTTTGGCGAGCTGGCGAC 2212309

QY 715 CCAGTGGGCTGATCCGCTGACCGCGCGAGCGCGCTGTTGCGGAAGAGTGGG 774  
Db 2212310 CCAAAGCGCGCCCTGAGACCGGATCTGGCGGAACATCTGGCGGTGGCGCCGAACAATGCG 2212369

QY 775 CCGCTGATCAGCAGGATCTTCTGCTG 802  
Db 2212370 GGGCTTCATGCTGAGAACCGCCAGCAG 2212397

## RESULT 7

US-09-252-991A-3537/c  
Sequence 3537, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 3537  
LENGTH: 1119  
TYPE: DNA  
ORGANISM: Pseudomonas aeruginosa  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (274)  
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.  
US-09-252-991A-3537

Query Match 3.9%; Score 39.8; DB 4; Length 1119;  
Best Local Similarity 53.5%; Pred. No. 0.073;  
Matches 83; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 715 CCACGTGGGCTGATCCGCTGACCGCGCGCGACCGCGCTGTTGCGGAAGAGTGGG 774  
Db 619 CCGCATGGGCTAGACACCGCTGCTCGCGCTGCGCGCGCGGCTTTCGGCGCGCAGCG 560

QY 775 CCGCTGATCAGCAGGATCTTCTGCTGGAGAAATTCGCGAGGGAGTGGGGGAGAA 834  
Db 559 CCAGCGCATCGCCCTGGCGCGCGCTGTACGGCGCGCGACCCCTGCTGCTCGACGA 500

QY 835 AACCATCTGACTACCGCGGAACACCCCGCGCATG 869  
Db 499 ACCCAACTCGAACCTCGACGACGCGGAGCATG 465

## RESULT 8

US-09-252-991A-3549  
Sequence 3549, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 3549

```
; LENGTH: 1581
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3549

Query Match      3.9%; Score 39.8; DB 4; Length 1581;
Best Local Similarity 53.5%; Pred. No. 0.088;
Matches 83; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 715 CCACGTGGCGTGCATCCGTGTCACGGCGCGGACGCGCGCTGTTGCCGAAGAGTGG 774
   |||||
DB 1372 CCGCATGGGTACGACACCGTGTCCGCGTCCGCGCGCGCGCTTCCGGGGCCAGCG 1431
   |||||

QY 775 CCGCTCATCACCGAGGATCTTCTGCTGGAGGAAATCCCGCAGGGGAGTGGGGCCGAGAA 834
   |||||
DB 1432 CCAGCGCATCGCCCTGCGCCGGCGGCTGTACGGCGCGCCGACCTGCTGTGCTCGACGA 1491
   |||||

QY 835 AACCACTCGACTACCGGAAACACCCGCGCATG 869
   |||||
DB 1492 ACCCACTCGAACCCTGACGACGCGCGGAGCATG 1526
   |||||

RESULT 9
US-09-252-991A-3557
; Sequence 3557, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3557
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; NAME/KEY: unsure
; LOCATION: (573)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-3557

Query Match      3.9%; Score 39.8; DB 4; Length 1947;
Best Local Similarity 53.5%; Pred. No. 0.098;
Matches 83; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 715 CCACGTGGCGTGCATCCGTGTCACGGCGCGGACGCGCGCTGTTGCCGAAGAGTGG 774
   |||||
DB 228 CCGCATGGGTACGACACCGTGTCCGCGTCCGCGCGCGCGCTTCCGGGGCCAGCG 287
   |||||

QY 775 CCGCTCATCACCGAGGATCTTCTGCTGGAGGAAATCCCGCAGGGGAGTGGGGCCGAGAA 834
   |||||
DB 288 CCAGCGCATCGCCCTGCGCCGGCGGCTGTACGGCGCGCCGACCTGCTGTGCTCGACGA 347
   |||||

QY 835 AACCACTCGACTACCGGAAACACCCGCGCATG 869
   |||||
DB 348 ACCCACTCGAACCCTGACGACGCGCGGAGCATG 382
   |||||

RESULT 10
US-09-252-991A-2233/c
; Sequence 2233, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
```

```
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2233
; LENGTH: 465
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2233

Query Match      3.8%; Score 39.2; DB 4; Length 465;
Best Local Similarity 50.5%; Pred. No. 0.07;
Matches 95; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 607 CACGTGCTGTGACCGAGGACCTGCTTATTGAGGCGCCATTGGTTTGAATGCGAAG 666
   |||||
DB 396 CACCTGTGTTCTCGACGAGATCGAAAGCATGCCGTTGGCGCAGCAGGTCAAGCTGCTGCG 337
   |||||

QY 667 CGACGAACAGTCCGCTACCTTGGAAAGGCCCGACCCGAAATCTGCGCATCCACGTGGCGGT 726
   |||||
DB 336 CGTCTCGACGAGCAGCAACTGGAGCGGCTCGGCTCGAACGAGATATCCACGTGACCT 277
   |||||

QY 727 CGATCCGCTGCACGGCGGAGCGCGGCTGGTTGCCGAAGAGTGGCGGCGCTGATCAC 786
   |||||
DB 276 GCGGCTGATTCCCGCAGCAACCGCCGCTGCTGCGCAAGACGTCGCGGACGCTTCCG 217
   |||||

QY 787 CGAGGATC 794
   |||||
DB 216 CGAGGACC 209
   |||||

RESULT 11
US-09-252-991A-2447
; Sequence 2447, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2447
; LENGTH: 852
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2447

Query Match      3.8%; Score 39.2; DB 4; Length 852;
Best Local Similarity 50.5%; Pred. No. 0.096;
Matches 95; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 607 CACGTGCTGTGACCGAGGACCTGCTTATTGAGGCGCCATTGGTTTGAATGCGAAG 666
   |||||
DB 64 CACCTGTGTTCTCGACGAGATCGAAAGCATGCCGTTGGCGCAGCAGGTCAAGCTGCTGCG 123
   |||||

QY 667 CGACGAACAGTCCGCTACCTTGGAAAGGCCCGACCCGAAATCTGCGCATCCACGTGGCGGT 726
   |||||
DB 124 CGTCTCGACGAGCAGCAACTGGAGCGGCTCGGCTCGAACGAGATATCCACGTGACCT 183
   |||||

QY 727 CGATCCGCTGCACGGCGGAGCGCGGCTGGTTGCCGAAGAGTGGCGGCGCTGATCAC 786
   |||||
DB 184 GCGGCTGATTCCCGCAGCAACCGCCGCTGCTGCGCAAGACGTCGCGGACGCTTCCG 243
   |||||
```

```
QY 787 CGAGGATC 794
Db 244 CGAGGACC 251

RESULT 12
US-09-252-991A-2528
; Sequence 2528, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2528
; LENGTH: 1359
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2529

Query Match 3.8%; Score 39.2; DB 4; Length 1359;
Best Local Similarity 50.5%; Pred. No. 0.12;
Matches 95; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 607 CACCGTCTCGTACCGAGGACCTGCTTATTGAGGCGCCATTGGTTTGAATGCGAAG 666
Db 729 CACCGTCTCTCGACGAGATCGAAGCATGCCGTGGCGCAGAGGTCAAGCTGCTGCG 788
QY 667 CGACGAACAGTCGCTACCTGGAAGCCCCGACCCGAATCTGCGCATCCACGTGGCGGT 726
Db 789 CGTCTCGAGAGAGACACTGGACGCGCTGGCTCGAACGAGATATCCACGTGCACT 848
QY 727 CGATCCGTCGACGGCGGCGGCGCGCTGGTTCGGAAGAGTGGCGCCGCTGATCAC 786
Db 849 GCGGGTGATTGCGGCGGACCAAGCCGACCTGCTGGCCGAGCAGCTGCGGACGCTTCCG 908
QY 787 CGAGGATC 794
Db 909 CGAGGACC 916

RESULT 13
US-09-252-991A-2391/c
; Sequence 2391, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 2391
; LENGTH: 1473
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2391

Query Match 3.8%; Score 39.2; DB 4; Length 1473;
Best Local Similarity 50.5%; Pred. No. 0.13;
Matches 95; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
```

```
QY 607 CACCGTCTCGTACCGAGGACCTGCTTATTGAGGCGCCATTGGTTTGAATGCGAAG 666
Db 649 CACCGTCTCTCGACGAGATCGAAGCATGCCGTGGCGCAGCAGGTCAAGCTGCTGCG 590
QY 667 CGACGAACAGTCGCTACCTGGAAGCCCCGACCCGAATCTGCGCATCCACGTGGCGGT 726
Db 589 CGTCTCGAGGAGCAGCAACTGGAGCGGCTCGGCTCGAACCAAGAGTATCCACGTGCACT 530
QY 727 CGATCCGTCGACGGCGGCGGCGCGCTGGTTCGGAAGAGTGGCGCCGCTGATCAC 786
Db 529 GCGGGTGATTGCGCGCAACCAAGCCGACCTGCTGGCCGGAAGCACGTGCCGAGGCTTCCG 470
QY 787 CGAGGATC 794
Db 469 CGAGGACC 462

RESULT 14
US-09-252-991A-8431
; Sequence 8431, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8431
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8431

Query Match 3.8%; Score 38.4; DB 4; Length 876;
Best Local Similarity 62.5%; Pred. No. 0.17;
Matches 60; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 693 GCCCGACCGCAATCTGCGCATCCAGTGGGCGGTGATCGCTGCACGGCGGAGCGG 752
Db 567 GCGACGGCCAGCGCGCTGAGCCTGGCGGTGCGGGGACCTGGTGTGGACGTGGCGGACG 626
QY 753 CGCTGTTGCCGAAGAGCTGCGCGCTGATCACCG 788
Db 627 CGCTGTCGACGGCGGCGCTGGTCCGCCAGGCGATCG 662
```

```
RESULT 15
US-09-252-991A-8415/c
; Sequence 8415, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8415
; LENGTH: 1002
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
```

US-09-252-991A-8415

Query Match 3.8%; Score 38.4; DB 4; Length 1002;  
 Best Local Similarity 62.5%; Pred. No. 0.18; 36; Indels 0; Gaps 0;  
 Matches 60; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
 Qy 693 GCCCGACCGGAATCTCGCATCCACGCTGGGCGTGGATCGCTGCACGGCGGACCGCG 752  
 Db 353 GCGACGCCAGCCGCTGAGCTGCGGCTGGCGGCGACCTGGTGGCTGGACGTGGCGGACG 294  
 Qy 753 CGCTGGTTGCCGAAGAGCTGGCGCGCTGATCACC 788  
 Db 293 CGCTGGTCGACGGCGCGCTGGCGGCGGCGATCG 258

Search completed: December 5, 2004, 05:50:14  
 Job time : 145 secs

## SUMMARIES

## ALIGNMENTS

## RESULT 1

US-09-738-626-1  
; Sequence 1, Application US/09738626

```

1 // Publication No. US20020197605A1
2 //
3 // GENERAL INFORMATION:
4 //
5 // APPLICANT: NAKAGAWA, SATOSHI
6 // APPLICANT: MIZOGUCHI, HIROSHI
7 // APPLICANT: ANDO, SEIKO
8 // APPLICANT: HAYASHI, MIKIRO
9 // APPLICANT: OCHIAI, KEIKO
10 // APPLICANT: YOKOI, HARUHIKO
11 // APPLICANT: TATEISHI, NAKOKO
12 // APPLICANT: SENOH, AKIHIRO
13 // APPLICANT: IKEDA, MASATO
14 // APPLICANT: OZAKI, AKITO
15 //
16 // TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
17 //
18 // FILE REFERENCE: 249-125
19 //
20 // CURRENT APPLICATION NUMBER: US/09/738,626
21 // CURRENT FILING DATE: 2000-12-18
22 //
23 // PRIOR APPLICATION NUMBER: JP 99/377484
24 // PRIOR FILING DATE: 1999-12-16
25 //
26 // PRIOR APPLICATION NUMBER: JP 00/159162
27 // PRIOR FILING DATE: 2000-04-07
28 //
29 // PRIOR APPLICATION NUMBER: JP 00/280988
30 // PRIOR FILING DATE: 2000-08-03
31 //
32 // NUMBER OF SEQ ID NOS: 7059
33 //
34 // SOFTWARE: Patent In ver. 3.0
35 //
36 // SEQ ID NO 1
37 //
38 // LENGTH: 3309400
39 //
40 // TYPE: DNA
41 //
42 // ORGANISM: Corynebacterium glutamicum
43 //
44 // US-09-738-626-1

```

Query Match 98.8%; Score 1011; DB 9; Length 3309400;  
Best Local Similarity 99.9%; Pred. No. 0;

Matches 1022; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 AGGCATCAAAACCCACAGCACAACACACAGAGCTGGCCAGATCTCCATCCGTGGTGAATA 60  
DB 592763 AGGCATCAAAACCCACAGCACAACACACAGAGCTGGCCAGATCTCCATCCGTGGTGAATA 592822  
QY 61 CATCGGTGTTGCAGATGCGACCGGATAGGTGATGACTCATGAGCACCACCAACAATCAC 120  
DB 592823 CATCGGTGTTGCAGATGCGACCGGATAGGTGATGACTCATGAGCACCACCAACAATCAC 592881  
QY 121 CATCACAGTCTCTAGAAACCCCAACCATCTTTGACGGCCCTGAAACCATCTACCGCTATGA 180  
DB 592882 CATCACAGTCTCTAGAAACCCCAACCATCTTTGACGGCCCTGAAACCATCTACCGCTATGA 592941  
QY 181 CTTGGCTGCGAAGGCAATCTTTGATGATGGGCTCACTCTGCTGTGCTGGATCAAGTGA 240  
DB 592942 CTTGGCTGCGAAGGCAATCTTTGATGATGGGCTCACTCTGCTGTGCTGGATCAAGTGA 593001  
QY 241 ACAATAGCAGGTGAAACCTGGCGACTGTTGAGATCGTGTGATGGCAGCAGCAACGT 300  
DB 593002 ACAATAGCAGGTGAAACCTGGCGACTGTTGAGATCGTGTGATGGCAGCAGCAACGT 593061  
QY 301 AGTCAATGCACTCACTCCATCTTTGCTTCCAAAGCGGTGACCTGCGGTGGGTGGAGT 360  
DB 593062 AGTCAATGCACTCACTCCATCTTTGCTTCCAAAGCGGTGACCTGCGGTGGGTGGAGT 593121  
QY 361 AGAGCAGCTCCGTTGCGGAGGAACACCGAATTAACGSCCCACGAGTGGAACA 420  
DB 593122 AGAGCAGCTCCGTTGCGGAGGAACACCGAATTAACGSCCCACGAGTGGAACA 593181  
QY 421 AGTCCGCGAGTTCTACGGCATCAAGCCTACACCTGTTGTTGGTCAGCATATGTTGG 480  
DB 593182 AGTCCGCGAGTTCTACGGCATCAAGCCTACACCTGTTGTTGGTCAGCATATGTTGG 593241  
QY 481 TTCTATTGCTGTTATTTGGGTGATTTGGGTGATTTCTGGGCGAGTGAGTCAAGCGCGT 540  
DB 593242 TTCTATTGCTGTTATTTGGGTGATTTGGGTGATTTCTGGGCGAGTGAGTCAAGCGCGT 593301  
QY 541 AGATAAGTGGCGAGATTTCAACGAGAGGGGAGAGCTCGATAAGCAATCAACCCCAAC 600  
DB 593302 AGATAAGTGGCGAGATTTCAACGAGAGGGGAGAGCTCGATAAGCAATCAACCCCAAC 593361  
QY 601 CCAGCCACCGTGTCTGTGACCGAGGACCTGCTTTATGAGGCGCCATTTGGTTTGAAT 660  
DB 593362 CCAGCCACCGTGTCTGTGACCGAGGACCTGCTTTATGAGGCGCCATTTGGTTTGAAT 593421  
QY 661 GCGAAGCAGCAACAGTCGCGCTACCTGGAAGCCCGGACCGAATCTGCGCATCCAGT 720  
DB 593422 GCGAAGCAGCAACAGTCGCGCTACCTGGAAGCCCGGACCGAATCTGCGCATCCAGT 593481  
QY 721 GGGCGTCCATCCGTGCAACGCGCGGACGCGCGCTGTTTCCGAAAGAGTCCGCGCCT 780  
DB 593482 GGGCGTCCATCCGTGCAACGCGCGGACGCGCGCTGTTTCCGAAAGAGTCCGCGCCT 593541  
QY 781 GATCACCGAGATCTTCTGCTGGAGGAATTCGCGAGGGGAGTGGCGGAGAAACCA 840  
DB 593542 GATCACCGAGATCTTCTGCTGGAGGAATTCGCGAGGGGAGTGGCGGAGAAACCA 593601  
QY 841 CATCGACTACCGGAAACACCGCGCATGCTCTCATGTGCTGTGGGTGACCTGTTTGA 900  
DB 593602 CATCGACTACCGGAAACACCGCGCATGCTCTCATGTGCTGTGGGTGACCTGTTTGA 593661  
QY 901 CACGACCGCAACTCAAGTGGTGGTCCATAGCAAGCCCGCAACCTGTTTCAAA 960  
DB 593662 CACGACCGCAACTCAAGTGGTGGTCCATAGCAAGCCCGCAACCTGTTTCAAA 593721  
QY 961 GGCACAAATGCGAAATGATGATGAGCATCTGAGGCTGAAATGATGCGCGTTCATCCGG 1020  
DB 593722 GGCACAAATGCGAAATGATGATGAGCATCTGAGGCTGAAATGATGCGCGTTCATCCGG 593781  
QY 1021 AAT 1023  
DB 593782 AAT 593784

## RESULT 2

US-09-738-626-643  
; Sequence 643, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIRO  
; APPLICANT: OCHIAI, KEIKO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TATEISHI, NAKO  
; APPLICANT: SENOH, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; APPLICANT: OZAKI, AKIO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738,626  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 00/159162  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: JP 00/280988  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 7059  
; SOFTWARE: Patent in ver. 3.0  
; SEQ ID NO 643  
; LENGTH: 900  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum  
US-09-738-626-643

Query Match 88.0%; Score 900; DB 9; Length 900;

Best Local Similarity 100.0%; Pred. No. 2.2e-283; Mismatches 0; Indels 0; Gaps 0;  
Matches 900; Conservative 0;

QY 101 ATGAGCAGCCCAACCAATCACCATCACAGTCTCTAGAAACCCGACCATCTTTGAGCGCCT 160  
DB 1 ATGAGCAGCCCAACCAATCACCATCACAGTCTCTAGAAACCCGACCATCTTTGAGCGCCT 60  
QY 161 GAAACCATCTACCGCTATGACCTGGCTGCGAGAGGCACTCTTGATGATGGGCTCATCT 220  
DB 61 GAAACCATCTACCGCTATGACCTGGCTGCGAGAGGCACTCTTGATGATGGGCTCATCT 120  
QY 221 GCTGTGCTGGATCAAGTGAACCAATAGCAGGTGAAACCTGGCGCACTGTTGAGATCGTG 280  
DB 121 GCTGTGCTGGATCAAGTGAACCAATAGCAGGTGAAACCTGGCGCACTGTTGAGATCGTG 180  
QY 281 GTGATGCAACCGCAACAGTCAATGCACTACCTCCATGTTTGGTTCGAAAGCGTG 340  
DB 181 GTGATGCAACCGCAACAGTCAATGCACTACCTCCATGTTTGGTTCGAAAGCGTG 240  
QY 341 ACCTGCGGTGGGTGGAGTAGAGCAGCTCCCGTTCGGAGGAAACCAACCGAAATTTAA 400  
DB 241 ACCTGCGGTGGGTGGAGTAGAGCAGCTCCCGTTCGGAGGAAACCAACCGAAATTTAA 300  
QY 401 CGGCCCCAGAGTGAACCAACAGTCCGCGAGTTCTACGGCATCAAGCACTACACCTGTTG 460  
DB 301 CGGCCCCAGAGTGAACCAACAGTCCGCGAGTTCTACGGCATCAAGCACTACACCTGTTG 360  
QY 461 TTGCTCAGCATATTGGTGGTCTTATTGCTGGTATTTGGGTGATTTCCGGTTTCACTGGG 520  
DB 361 TTGCTCAGCATATTGGTGGTCTTATTGCTGGTATTTGGGTGATTTCCGGTTTCACTGGG 420  
QY 521 CCAGTGGACTCACGCGCGGTAGATAAGGTGCGGAGATTTCAACGCGAGGGGAGACGTCG 580  
DB 421 CCAGTGGACTCACGCGCGGTAGATAAGGTGCGGAGATTTCAACGCGAGGGGAGACGTCG 480  
QY 581 ATAGCAATCAACCCCAACCCCGACCGCTGCTGACCGAGGACCTGCTATTGAG 640  
DB 593782 AAT 593784



Db 481 ATAGCAATCAACCCACCCACCCACCGTCTCGTGACGAGGACCTGCTATTGAG 540  
QY 641 GCGCATTTGTTTGAATGGAAGACGACGACGACGACGACGACGACGACGACGAC 700  
Db 541 GCGCATTTGTTTGAATGGAAGACGACGACGACGACGACGACGACGACGACGAC 600  
QY 701 CGGAATCTGCGCATCCAGTGGGCTGATCGCTGACGCGGCGGACGCGCTGTT 760  
Db 601 CGGAATCTGCGCATCCAGTGGGCTGATCGCTGACGCGGCGGACGCGCTGTT 660  
QY 761 GCGGAAGAGCTGCGCGCTGATCACCGAGGATCTTCGCTGGAGGAAATCCGCGAGG 820  
Db 661 GCGGAAGAGCTGCGCGCTGATCACCGAGGATCTTCGCTGGAGGAAATCCGCGAGG 720  
QY 821 GAGTGGGCGGAGAAACACCATGACACTACCGGAAACCGGCGGATGCTCATGTG 880  
Db 721 GAGTGGGCGGAGAAACACCATGACACTACCGGAAACCGGCGGATGCTCATGTG 780  
QY 881 CTGTGGGTGACCTGTTTGACACCGACGACAACTCAACGTTGGGTGCCATAGCAAGCC 940  
Db 781 CTGTGGGTGACCTGTTTGACACCGACGACAACTCAACGTTGGGTGCCATAGCAAGCC 840  
QY 941 GCGGAACCTGTTTTCACAGGACAAATGCCGAATGTAGTACATCTGACGCTGAAA 1000  
Db 841 GCGGAACCTGTTTTCACAGGACAAATGCCGAATGTAGTACATCTGACGCTGAAA 900

RESULT 3  
US-09-738-626-640  
; Sequence 840, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIRO  
; APPLICANT: OCHIAI, KEIKO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TATEISHI, NAOKO  
; APPLICANT: SENOH, AKIHIRO  
; APPLICANT: IKEDA, MAGATO  
; APPLICANT: OZAKI, AKIO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738,626  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 00/159162  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: JP 00/280988  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 7059  
; SOFTWARE: PatentIn ver. 3.0  
; SEQ ID NO 640  
; LENGTH: 3567  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum  
US-09-738-626-640

Query Match 8.7%; Score 89; DB 9; Length 3567;  
Best Local Similarity 99.0%; Pred. No. 7.6e-18;  
Matches 100; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 AGGCATCAACCCACGACGACACCAACGACGACGACGACGACGACGACGACGAC 60  
Db 3468 AGGCATCAACCCACGACGACACCAACGACGACGACGACGACGACGACGACGAC 3527  
QY 61 CATCGGTGTTGCACAGATGGACCGCATAGTGATGACTCA 101  
Db 3528 CATCGGTGTTGCACAGATGGCA-CGCATAGTGATGACTCA 3567

RESULT 4  
US-10-389-647-53  
; Sequence 53, Application US/10389647  
; Publication No. US20040033549A1  
; GENERAL INFORMATION:  
; APPLICANT: GREENBERG, E. Peter  
; APPLICANT: SCHUSTER, Martin  
; APPLICANT: LOSTROH, Candi  
; TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA  
; FILE REFERENCE: UIZ-038CP  
; CURRENT APPLICATION NUMBER: US/10/389,647  
; CURRENT FILING DATE: 2003-03-14  
; PRIOR APPLICATION NUMBER: 09/653730  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/153022  
; PRIOR FILING DATE: 1999-09-03  
; NUMBER OF SEQ ID NOS: 710  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 53  
; LENGTH: 1782  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-10-389-647-53

Query Match 4.4%; Score 44.6; DB 16; Length 1782;  
Best Local Similarity 52.4%; Pred. No. 0.0019;  
Matches 98; Conservative 0; Mismatches 89; Indels 0; Gaps 0;  
QY 671 GAACAGTCCGCTACCTGGAAGCCCGACCCGCAATCCGATCCACGTCGGCGTCGAT 730  
Db 1318 GAGCGCGCGCGCTGCGCGGGTCCATGAATGTCCTCGCGCTCGCGAGGGCTACGAC 1377  
QY 731 CCCTGTCACGCGCGGACGCGCGCTGCTGGTTCGCGAAGAGCTGCGCGCTGATCACCGAG 790  
Db 1378 ACCGTGCTCGGCTCGCGCGCGCGCGCTTCGCGCGCGCAGCGCGCATCGCCCTG 1437  
QY 791 GATCTTCGCTGAGGAAATTCGCGAGGGAGTGGGGGAGAAAACCACTCGACTAC 850  
Db 1438 GCCCGGCGCTGTACGCGCGCGCGCGCTGCTGCTGACGACCACTCGAACCTC 1497  
QY 851 CGCGAAA 857  
Db 1498 GACGACA 1504

RESULT 5  
US-10-156-761-1788  
; Sequence 1788, Application US/10156761  
; Publication No. US20030119016A1  
; GENERAL INFORMATION:  
; APPLICANT: OMURA, SATOSHI  
; APPLICANT: IKEDA, HARUO  
; APPLICANT: ISHIKAWA, JUN  
; APPLICANT: HORIKAWA, HIROSHI  
; APPLICANT: SHIBA, TADAYOSHI  
; APPLICANT: SAKAKI, YOSHIYUKI  
; APPLICANT: HAITORI, MASAHIRA  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-262  
; CURRENT APPLICATION NUMBER: US/10/156,761  
; CURRENT FILING DATE: 2002-05-29  
; PRIOR APPLICATION NUMBER: JP 2001-204089  
; PRIOR FILING DATE: 2001-05-30  
; PRIOR APPLICATION NUMBER: JP 2001-272697  
; PRIOR FILING DATE: 2001-08-02  
; NUMBER OF SEQ ID NOS: 15109  
; SEQ ID NO 1788  
; LENGTH: 2088  
; TYPE: DNA  
; ORGANISM: Streptomyces avermitilis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2088)



Qy	526	GACCTGCTTATTAGAGCGCCATTGTGTTTGAATGCGAAGCGACGAACATGTCGCGCTAC	685
Db	28479	GCCTCGGAAGAGCGGTGAGACGCGCGACCTGCCGACATCGCTTACACGTGCGAG	28538
Qy	686	CTGGAAGGCCCGACCCGAATCTGCGATCCACGTGGCGTCGATCCGCTGCACGGCCG	745
Db	28539	GTCGGCGCGAGCGCATGCCGACCGGTTCCGCGTGGCGTCGACACGCTTCCGCCCTG	28598
Qy	746	GAGCCGCGCTGTTGCTCCGAAAGAGCTGCGCCGCTGATCACCGAGG	791
Db	28599	GTGACGCGCTGACGCCCTGCGGCTCGGACGCGGCTGCCCGCG	28644

## RESULT 9

```

US-10-156-761-3557/c
; Sequence 3557, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 3557
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(807)
US-10-156-761-3557

```

	Query Match	4.1%;	Score 41.8;	DB 15;	Length 807;
	Best Local Similarity	53.3%;	Pred. No. 0.011;		
	Matches	88;	Conservative	0;	Mismatches 77; Indels 0; Gaps 0;
QY	670	CGAACACTCGCGCTACCTGGAAGCCCGACCCGAACTCGCGATCACCTGGGGCGTCGA	729		
Db	166	CGATCAGCGGGTGACGTTCGCGGGGCGGCAGCCAGGTCGCGGATCGGGCGGGGTCCC	107		
QY	730	TCGCGCTGCACGGCGCGGACGCGCGCTGCTTCCGAAAGAGTGGCGCGCCTGTATCACCGA	789		
Db	106	GGGSCACTCGGGGACGCGGCGCCAGAGGTCGGGAAGGGCGGCGCGGTGATCCGCGT	47		
QY	790	GGATCTCTCGCTGGAGGAAATTCGCGCAGGGGAGTGGGGCGAGAA	834		
Db	46	GGGCGAGGTACTGGCTGGGATCCAGGTGGGACGGGGCGGGCA	2		

## RESULT 10

```

US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

```

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; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match 4.1%; Score 41.8; DB 15; Length 9025608;
Best Local Similarity 53.3%; Pred. No. 0.53; 77; Indels 0; Gaps 0;
Matches 88; Conservative 0; Mismatches 0;

Qy 670 CGAACAGTGCAGCTACTCGAAGGCCCGACCCGGAATCTGCGAATCCACGTGGCGTCCA 729
Db 4421279 CGATCAGGCGGTGACGTTTCCGGGGCCCGACGCCAGGTTCGCGCGAGTCCC 4421338

Qy 730 TCCGCTGCACGGCGGAGCCCGCTGGTTCCCGAAGAGCTCCGCGCTCATCACCGA 789
Db 4421339 GGGCGAGCTCGGGAGACCGGGCCAGCAGGTTCGCGAAGGGCGGGCGGTGATCCGCT 4421398

Qy 790 GGATCTTCGCTGGAGAAATTCCTCCAGGGAGTGGGCGAGAA 834
Db 4421399 GGGCAGGTACTGGCTGGGATCCAGCTGGGACCGGCGCGGGCA 4421443

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## RESULT 11

```

US-10-282-122A-31290
Sequence 31290, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIORITY APPLICATION NUMBER: 60/191,078
PRIORITY FILING DATE: 2000-03-21
PRIORITY APPLICATION NUMBER: 60/206,848
PRIORITY FILING DATE: 2000-05-23
PRIORITY APPLICATION NUMBER: 60/207,727
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: 60/230,335
PRIORITY FILING DATE: 2000-09-06
PRIORITY APPLICATION NUMBER: 60/230,347
PRIORITY FILING DATE: 2000-09-09
PRIORITY APPLICATION NUMBER: 60/242,578
PRIORITY FILING DATE: 2000-10-23
PRIORITY APPLICATION NUMBER: 60/253,625
PRIORITY FILING DATE: 2000-11-27
PRIORITY APPLICATION NUMBER: 60/257,931
PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: 60/267,636

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; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31290
; LENGTH: 1392
; TYPE: DNA
; ORGANISM: Pseudomonas putida
; US-10-282-122A-31290

Query Match
Best Local Similarity 4.1%; Score 41.6; DB 16; Length 1392;
Matches 107; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 651 GTTTTGAATGCGAAGCAGACAGTCGCGCTACCTGGAAGCCCGCCGAGATCTGC 710
Db 530 GGTTTGAATGCTCAGCGCGCACTATGAGCGCCTGTGCTCGACTCCGCAAGCGCACCAAC 589

QY 711 GCATCCACGTGGCGGTGATCCGCTGCACGCGCGGACGCGCGCTGTTGCCGAAGAGC 770
Db 590 GCATGCCACGTGGCGAGCGCGCGCTGCGCGCACCACTACCGATCGACCGTGAAGTGA 649

QY 771 TGCGCCCGCTGATCACCAGAGATCCTTCGTGTGAGAGAAATTCGCGAGGGAGTGGGGCG 830
Db 650 CCTGCAAGCTGCTGGGCTTTGAAGCCGTGCGCGCAACTCGCTGGATGGCGTGTGCGACC 709

QY 831 AGAAACACCATGACTACCGCGGACCAACCCGCGC 866
Db 710 GTGATTTCGCATCGAATTCGCGCCGCTGCCAGCG 745

RESULT 12
US-10-470-565-1/c
; Sequence 1, Application US/10470565
; Publication No. US20040126870A1
; GENERAL INFORMATION:
; APPLICANT: Societe des Produits Nestle S.A.
; TITLE OF INVENTION: MCC2705 - the genome of a Bifidobacterium
; FILE REFERENCE: 80290/WO
; CURRENT APPLICATION NUMBER: US/10/470,565
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: EP 01102050.0
; PRIOR FILING DATE: 2001-01-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2256646
; TYPE: DNA
; ORGANISM: Bifidobacterium longum
; US-10-470-565-1

Query Match
Best Local Similarity 4.1%; Score 41.6; DB 17; Length 2256646;
Matches 86; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 696 CCGACCCGATCTCGGATCCAGTCGGGCTGATCCGCTGACCGAGGATCTTCGCTGGAGAAATTC 755
Db 1331150 CTTTCCCGGATCTGTGTATCAGTGCGCTGCAACCGCAAGCGCGCAGGAGA 1331091

QY 756 TGGTTGCCGAAGAGCTGGCGCGCTGATCACCAGGATCTTCGCTGGAGAAATTC 815
Db 1331090 AGATGGGCATCGCCCTTCTCCAAAGTGGCGGAGAGATCCGACTTCCAGGTACGACCG 1331031

QY 816 CAGGGGAGTGGGGGAGAAACCAACCATCGACTACCGCA 855
Db 1331030 ACGAAGAGTCGGCGCACACCTGTATCGCGGATGGCGCA 1330991

RESULT 13
US-10-156-761-3188
; Sequence 3188, Application US/10156761

```

```

; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 3188
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(711)
; US-10-156-761-3188

Query Match
Best Local Similarity 4.0%; Score 41.4; DB 15; Length 711;
Matches 99; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 660 TCGAAGCGCAGACAGTCGCGCTACCTGGAAGCCCGCCGAGTCTGGCATCCAGC 719
Db 464 TCGCGCGCGACGTCCAGATGACGAGAACTACCGCCGACCTCCGACAAGCCCCCTGGACG 523

QY 720 TGGCGGTGATCCGCTGCACGCGCGGACGCGCGCTGGTTGCCGAAGAGCTGCGCGCC 779
Db 524 TGGCGGTGATCCGCGCTGCGCGGACGAGGAGGAGTGTGTCGACGCGGAGCATCCGCC 583

QY 780 TGATCACCAGGATCTTCGCTGAGGAGAAATTCGCGAGGGAGTGGGGCGGAGAAACCA 839
Db 584 AGTGGCGCGGCGGACCAACCGCCGACTTCCGACGCGGAGCTGCGAGCGCGGACACATGT 643

QY 840 CCATCGACTACCGCG 854
Db 644 ACCTGGCGGACGCGC 658

RESULT 14
US-09-712-363-144/c
; Sequence 144, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; INTERACTIONS OF PROTEINS BY COMPARATIVE ANALYSIS
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14

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; PRIOR APPLICATION NUMBER: 60/134,092  
; PRIOR FILING DATE: 1999-05-14  
; PRIOR APPLICATION NUMBER: 60/165,124  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/165,086  
; PRIOR FILING DATE: 1999-11-12  
; NUMBER OF SEQ ID NOS: 292  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 144  
; LENGTH: 3297  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
US-09-712-363-144

Query Match 4.0%; Score 41.4; DB 9; Length 3297;  
Best Local Similarity 55.1%; Pred. No. 0.028;  
Matches 81; Conservative 0; Mismatches 66; Indels 0; Gaps 0;  
QY 663 GAAGCGACGACAGTCGGCTACCTGGAAGCCCCCGACCGCAATCTGCGATCCACGTGG 722  
Db |||||  
2162 GACGCGACGACACCGCCGCCATGAACCGGCCACGATCGGTACCGGGGCTGTGTCAGC 2103  
QY 723 GCGTCGATCCGCTGCACGCGCGGACGCGCGCTGTTCCGAAAGAGCTGGCGCGCTGA 782  
Db |||||  
2102 GCGCGGATCAGCGCCCTTCGCCGCGCGCGCGGCGGCGGAAGTCAGCCAGCCGCGCATAG 2043  
QY 783 TCACGAGAGATCCTTCGTTGGAGGAAA 809  
Db |||||  
2042 CCGCGCGGATCGCAACAGGGCGAAA 2016

RESULT 15  
US-10-437-963-82252  
; Sequence 82252, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 82252  
; LENGTH: 1359  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_816C.1  
US-10-437-963-82252

Query Match 4.0%; Score 41; DB 17; Length 1359;  
Best Local Similarity 49.8%; Pred. No. 0.026;  
Matches 104; Conservative 0; Mismatches 105; Indels 0; Gaps 0;  
QY 699 ACCCGAATCTGGCATCCACGTCGGCGTCGATCCGCTCACGCGCGGACCGCGCGCTGG 758  
Db |||||  
602 ACGCGACCGCGGCGCATGGTGTCCACGAAGGAACACAGAGTGGAGGCGCGCATGG 661  
QY 759 TTGCGAAGAGTGGCGCGCTGATCACCAGGATCTTCGCTGGAGGAATTCGCCGAG 818  
Db |||||  
662 CGTCCCGGTTGGCGCGCGCGTTCACGGCGTACGCGCGCGGTGGCGGATGCCGTACG 721  
QY 819 GGGAGTGGGGGAGAAAACACCATCGACTACCGGAAACACCGCGGATGGCTCTCATG 878  
Db |||||  
722 AGGAGAGGGTTCGGGGACGACCTCTACTCTTCGACGCGCGCGCGCGCGCTCC 781

QY 879 TGCTGTGGGTGACCTGGTTTGACACCGAC 907  
Db 782 ACGTGCTCATGCTCGGCTCGTACCGCGAC 810

Search completed: December 5, 2004, 07:18:09  
Job time : 651 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 3, 2004, 15:32:36 ; Search time 40 seconds  
(without alignments)  
497.385 Million cell updates/sec

Title: US-09-605-703B-2

Perfect score: 1566

Sequence: 1 MSTQITITVLETAIFDGP.....AETLVHKAQRNVIEHLTK 300

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A.COMB.pap:\*  
2: /cgn2\_6/ptodata/1/iaa/5B.COMB.pap:\*  
3: /cgn2\_6/ptodata/1/iaa/6A.COMB.pap:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102.5	6.5	3892	4	US-09-328-352-5503
2	94.5	6.0	284	4	US-09-252-991A-30616
3	90.5	5.8	1297	4	US-09-107-532A-4552
4	90	5.7	3816	3	US-09-428-517-3
5	88.5	5.7	358	4	US-09-252-991A-20171
6	88.5	5.7	544	4	US-09-489-039A-13133
7	87.5	5.6	163	4	US-08-477-135A-130
8	87	5.6	818	4	US-09-252-991A-31752
9	86.5	5.5	7257	3	US-09-335-409-5
10	86.5	5.5	7257	3	US-09-568-102-5
11	86.5	5.5	7257	3	US-09-567-969-5
12	86.5	5.5	7257	3	US-09-568-480-5
13	86.5	5.5	7257	3	US-09-568-486-5
14	86.5	5.5	7257	3	US-09-568-472-5
15	86.5	5.5	7257	3	US-09-567-899-5
16	85.5	5.5	569	4	US-09-107-532A-6689
17	85	5.4	372	4	US-09-252-991A-26719
18	85	5.4	420	4	US-09-328-352-5997
19	84.5	5.4	256	4	US-09-134-000C-4449
20	84.5	5.4	1070	4	US-09-961-403-3
21	84	5.4	2080	4	US-08-382-552-2
22	83.5	5.3	440	4	US-09-252-991A-22913
23	83.5	5.3	1040	4	US-09-711-164-442
24	83.5	5.3	1040	4	US-09-492-709A-282
25	82.5	5.3	263	4	US-09-252-991A-30502
26	82.5	5.3	389	4	US-09-134-000C-5382
27	82.5	5.3	640	4	US-09-533-029-84

28	82.5	5.3	1043	4	US-09-252-991A-31111	Sequence 31111, A
29	82.5	5.3	1618	1	US-07-853-913-4	Sequence 4, Appli
30	82.5	5.3	1618	4	US-09-338-092-1143	Sequence 1143, A
31	82	5.2	180	4	US-09-248-796A-19416	Sequence 19416, A
32	81.5	5.2	903	3	US-09-193-562D-46	Sequence 46, Appl
33	81.5	5.2	903	4	US-10-055-412B-46	Sequence 46, Appl
34	81.5	5.2	1963	4	US-09-583-110-5243	Sequence 5243, A
35	80.5	5.1	501	4	US-09-252-991A-25173	Sequence 25173, A
36	80.5	5.1	731	1	US-08-014-897-2	Sequence 2, Appli
37	80.5	5.1	731	1	US-08-731-716-2	Sequence 2, Appli
38	80	5.1	347	4	US-09-198-452A-488	Sequence 488, App
39	80	5.1	688	4	US-09-252-991A-27096	Sequence 27096, A
40	79.5	5.1	336	4	US-09-543-681A-5330	Sequence 5330, A
41	79.5	5.1	389	4	US-09-252-991A-18644	Sequence 18644, A
42	79.5	5.1	499	4	US-09-252-991A-17198	Sequence 17198, A
43	79.5	5.1	703	4	US-09-252-991A-20065	Sequence 20065, A
44	79.5	5.1	1190	4	US-09-252-991A-21474	Sequence 21474, A
45	79.5	5.1	1751	3	US-09-136-574A-44	Sequence 44, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-328-352-5503  
; Sequence 5503, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 5503  
; LENGTH: 3892  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-5503

Query Match 6.5%; Score 102.5; DB 4; Length 3892;  
Best Local Similarity 22.5%; Pred. No. 0.76;  
Matches 77; Conservative 29; Mismatches 115; Indels 121; Gaps 15;

Qy	2	STQITITVLETAIFDGPETIYRDAAAGILGDGWAHSAVLDQVKQIA-----50
Db	612	STVTVTYPNGDTATVAGPDG--SWSVPNPLNDG-----DEVEAIATDPAGNPSLPG 662
Qy	51	-----GENWPVEIVVDG--TDNVVVALTSMFASKGYTCGGVGVGVEAPPVAEPPKIKR 101
Db	663	TATVDVAGNTDGVNFTVDSVTADNVINASE---ASGNVTVTGVLKNVPADAN-----713
Qy	102	PTSGKQVRFYGIKPLHLLLSIL-----VGSIAGIWVI---SGFTGFVDSRPVD 148
Db	714	-----TWVTWINGQYTTATVDSCTAGTWTVSVPGLTADAKTIDA 755
Qy	149	KVABISTQGETISNQPOQPTVLVTEDLLEAPGFEMRSEQSRYLEGPPNLIHVG 208
Db	756	KVTFTDAAGNSSVN-----DTQYTTIDTTAPDAPV---786
Qy	209	VDPHGADAAALVAEELRLIT---EDPSLEEIPAGEWGEKTTIDYRETPG---DGSHVLWV 263
Db	787	INPVNGTDPITGTAEPGSIIVTYPDGSTTTTVVAGPDGTWTV---PNPLNDGDK---V 839
Qy	264	TWFTDTRQLN-----VGCHSKAAETLVHKAQRNVI 294
Db	840	TAIATDPAGNPSLPGTATVDVAGPNTDGVNFTVDSVTADNVI 881

##### RESULT 2

US-09-252-991A-30616  
; Sequence 30616, Application US/09252991A

```

; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30616
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-30616

Query Match      6.0%; Score 94.5; DB 4; Length 284;
Best Local Similarity 21.1%; Pred. No. 0.078;
Matches 51; Conservative 39; Mismatches 79; Indels 73; Gaps 10;

QY 39 HSAVLQVQKIAGENWTVIVVDGTDNVN-ALTSMFASKGVTGCGVGVEAPPVAEPPP 97
DB 67 NAAVLSRRRYTAGHSCTP-----HGMSMLHRLLSLMTASALVGLGCAL-SPQQLDPOP 120
QY 98 KIKRPTSGKQVRQYGIKPLHLLVSVLSIAGIWIISGFTGP-----VD 143
DB 121 VLKGP-----LTAVGHQPVVVKVVDGRPGSLGTRGGLVADTSTLT 162
QY 144 SRPVDKVAEISTQGETSIS-----NQPO-----POPTVLVTEDLLIE 180
DB 163 VRSEDDVFKLQAQAEATVRLVILGYTPSANAYNAPQLILTLAELKYQSPKGVVYV-----Q 217
QY 181 APFGFVRSDEOS---RYLEGPDNLRHVGDPLHGAADALVAEELRLIIT---BDPSL 234
DB 218 ADITATFADVQNSRRYTRYGASLNCRFGMAPNQATNSKLVSEVLSDALTRVFXDPTI 277
QY 235 EE 236
DB 278 AQ 279

RESULT 3
US-09-107-532A-4552
; Sequence 4552, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997

; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4552:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1297 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...1297
; SEQUENCE DESCRIPTION: SEQ ID NO: 4552:
; US-09-107-532A-4552

Query Match      5.8%; Score 90.5; DB 4; Length 1297;
Best Local Similarity 23.1%; Pred. No. 2.6;
Matches 71; Conservative 28; Mismatches 100; Indels 109; Gaps 17;

QY 45 QVKIAGENWTVIVVDGTDNVNVALTS-----MFASKGVTGCGVGVEAPPV 92
DB 984 QLKQTGEENWOYLTYTTDEEDRLWVAFYNTFYREIRVKLDHGHHTLDGAGFDIRKV 1043
QY 93 AB-----BPPKIKR-PTSGKQVRQYGI-----KPLHLLVSVLSI 128
DB 1044 GDSFPPLVAYTGNPLEPEESKRLPGIGYFYRAVGVEKYVDLNYDQPLHLSI----- 1096
QY 129 IAGIWIISGFTGPDVSRPDKVAEISTQGE-----TSISNQPOPOP-----TVLV 173
DB 1097 --GEYEVESVAPNGYRLSDQVQFALNEEGKFIETDVIETAPLPEGEYIIDGVLOV 1154
QY 174 T-EDLLIAPFGFWRSD--QSRYLEG-----PDPN-LRIHV 207
DB 1155 TLEDEL--APIDLELLKIDSNNRLEGAEPFSEKQNSAGEYIEGGAPDPNDSLSFN 1212
QY 208 GVDPLHGA---DAALVAEELRL-----ITDPSLEE---IPAGEWGE-KTTIDY- 250
DB 1213 ASDLLGVYRIKEVKSPDSYRKLPGYFILEISYREEPDIENDRVVPGKEAGTLKVEISYY 1272
QY 251 ----RETP 254
DB 1273 PNEEAETP 1280

RESULT 4
US-09-428-517-3
; Sequence 3, Application US/09428517
; Patent No. 6251636
; GENERAL INFORMATION:
; APPLICANT: Betlach, Mary C.
; APPLICANT: Shah, Sanjay Krishnakant
; APPLICANT: McDaniel, Robert
; APPLICANT: Tang, Li
; TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 30062-20029.00
; CURRENT APPLICATION NUMBER: US/09/428,517
; CURRENT FILING DATE: 1999-10-28
; EARLIER APPLICATION NUMBER: 60/120,254
; EARLIER FILING DATE: 1999-02-16
; EARLIER APPLICATION NUMBER: 60/106,100
; EARLIER FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 3816
; TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Recombinant
; OTHER INFORMATION: Oleandolide PKS
US-09-428-517-3

Query Match          5.7%; Score 90; DB 3; Length 3816;
Best Local Similarity 20.9%; Pred. No. 18;
Matches 71; Conservative 30; Mismatches 129; Indels 110; Gaps 16;

QY 17 FDGPETIVRY--DLAAEGIL-----DGWA-HSAVLDOVKIOIAGEN-----53
DB 2660 FQGLHTARHGDDVVAEVALPEGIPADGIALHPALDDAAVQAVLGSGFVEDPGGVYLPFL 2719
QY 54 WPTVEIVVDGT-----DNVVALTSMFASKGVTCGGVGVAPPVA-----93
DB 2720 WSDVTLHATGATSLRVRVSPAGPDTVALADPAGPVATGALRLRTTSAQALARAGS 2779
QY 94 -----EPPKIKPTSGKQVQFYGIKPLHLLVLSILVSGIAGIWIISGFTGPV 142
DB 2780 ABHAMFRVWEVSGAADCRCGGAGGTTTGERAAE-----AGAAAGTWAVLGRVPA 2832
QY 143 DSR-----PVD--KVAEISTOGETSISNQPPQPTVLVTEDLL-----IE 180
DB 2833 AVRTMGVDVVTALDTPDHPADPQSLADLAALGDT-----VPDVVVVTSLLSLASGAD 2884
QY 181 APFGFEMR--SDEQSRYLEGPDNLRHVGVDPPL-----HGAD-AALVAEELRLIIT 229
DB 2885 SPLGNRPRTAAEQDTAATVAGVSHALHAALDLVQAMLADEHRTASRLVLVTRHMTVAE 2944
QY 230 EDPSLEEIPAGWEKTKTIDYRETPG-----DGSHVLW 262
DB 2945 SDPEPDLLAPVWGLVRSQAQ-AENPGREVLADIDGDEASW 2983

RESULT 5
US-09-252-991A-20171
; Sequence 1071, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20171
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20171

Query Match          5.7%; Score 88.5; DB 4; Length 358;
Best Local Similarity 24.1%; Pred. No. 0.53;
Matches 56; Conservative 30; Mismatches 81; Indels 65; Gaps 14;

QY 87 VEAPP--VAEPPP--KIKRPTSGKQVQFYGIKPLHLLVLSILVSGIAGIWIISGFTGPV 142
DB 5 IRAPPNLSAQPPRGRLEAPTSQP--RKAY-----CSGLTSGNWLA-----44
QY 143 DSRPVDKVAEISTOGETSISNQPPQPTVLVTEDLLTEAPGFEMRDEQSRYLEGPDEN 202
DB 45 EHRAGREADREAGG---HVQPHQPVVLALEHRLVRAERGLGVGD-----VVHEEP- 94
QY 203 LRIHVGVDPLHGAD-----AALVAEELRLITEDPSLEEIPAGWEKTKTIDYR 251
DB 95 -----GRDHYGDERHDPDAGVLPQATVAEELRLAAEG---AEQAAGHRQRHGLHHR 146
```

```
QY 252 ET-----PG-----DGSHVLVWTFDTRQLNVGCHSKAAETLVHKAQCRNVIEH 296
DB 147 DAEVAEPGIAEGGALLALRIEAD-----IG-HARGEVAAAEAEQRDQGEH 193

RESULT 6
US-09-489-039A-13133
; Sequence 13133, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breston et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13133
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (519)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-489-039A-13133

Query Match          5.7%; Score 88.5; DB 4; Length 544;
Best Local Similarity 24.6%; Pred. No. 1.1;
Matches 31; Conservative 19; Mismatches 41; Indels 35; Gaps 6;

QY 179 IEAPFGFEMRDEQSRYLEGPDNLRHVGVDPPLH-GADA---ALVAEELRLITEDPSL 234
DB 198 LQGMFAFALYDSEKDAYLIGRD-----HTGIPLVYMGHDEHGNFYVASEMKALVPVCRTI 252
QY 235 EEIIPAGEW-----GEKTTIDYRETQDGGSHVLVWTFDTRQLNVGCHSKAAETLVHKAQ 289
DB 253 KEFPAGSYLWSDGEIRQYQRD-----WFDYD-----AVKDNVTDKNE 291
QY 290 CRNVIE 295
DB 292 LRQALE 297

RESULT 7
US-09-477-135A-130
; Sequence 130, Application US/09477135A
; Patent No. 6572865
; GENERAL INFORMATION:
; APPLICANT: Nano Francis
; TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
; FILE REFERENCE: Immunostimulatory Peptides
; FILE REFERENCE: 52888
; CURRENT APPLICATION NUMBER: US/09/477,135A
; CURRENT FILING DATE: 2000-01-03
; PRIOR APPLICATION NUMBER: 08990823
; PRIOR FILING DATE: 1997-12-15
; PRIOR APPLICATION NUMBER: US 96/10375
; PRIOR FILING DATE: 1996-06-14
; PRIOR APPLICATION NUMBER: 60/000,254
; PRIOR FILING DATE: 1995-06-15
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 130
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-477-135A-130

Query Match          5.6%; Score 87.5; DB 4; Length 163;
Best Local Similarity 23.3%; Pred. No. 0.19;
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QY 119 -----LLVLSILVG-----SIAGIWIISGFTGPDVSRPVDKVAE 152  
Db 2329 KPTLLGLLPACLPAPAEPTLLASLRAGREAAAGVLEALGRLWAAG-----S 2374  
QY 153 ISTQGETSISNQPOQPTVLVTEDLLIEAPFGFEMRSDQSRYLEGPDNLRHVGVDPL 212  
Db 2375 VSWPGVFPTAGRRVPLPTV-----PW-----QQRQYWPDIPEDSRRHAAADPT 2417  
QY 213 HGADAALVAEELRLITEDPSLEEIPAGEW 242  
Db 2418 QGWFYRVDWPEIPRSLOKS---EEASRGSW 2444

## RESULT 11

US-09-567-969-5  
; Sequence 5, Application US/09567969  
; Patent No. 6355457  
; GENERAL INFORMATION:  
; APPLICANT: Schupp, Thomas  
; APPLICANT: Ligon, James  
; APPLICANT: Molnar, Istvan  
; APPLICANT: Zirkle, Ross  
; APPLICANT: Cyr, Devon  
; APPLICANT: Goerlach, Joern  
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES  
; FILE REFERENCE: 4-30582A  
; CURRENT APPLICATION NUMBER: US/09/567,969  
; PRIOR FILING DATE: 2000-05-10  
; PRIOR FILING DATE: 1999-06-17  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 7257  
; TYPE: PRT  
; ORGANISM: Sorangium cellulosum  
US-09-567-969-5

Query Match 5.5%; Score 86.5; DB 3; Length 7257;  
Best Local Similarity 19.3%; Pred. No. 1.3e+02;  
Matches 52; Conservative 31; Mismatches 76; Indels 111; Gaps 11;  
QY 49 IAGENWPTVEIVDGTNDVNNALTSMFASKGVTCCGGVGE-----APPVAEEPPKI-- 99  
Db 2210 IAAVNGPE-QVVIAGVEQVQAIAAGFAARGARTKRLHVSHASHSPLEPMLEEFGRVAA 2268  
QY 100 ----KRPT-----SGK-----QVRQFYGIKPLH----- 118  
Db 2269 SVTYRRPSVLSNLGKVVADLSAPGYWYRVHREAVRFADGVKALHEAGAGTFFVEVGP 2328  
QY 119 -----LLVLSILVG-----SIAGIWIISGFTGPDVSRPVDKVAE 152  
Db 2329 KPTLLGLLPACLPAPAEPTLLASLRAGREAAAGVLEALGRLWAAG-----S 2374  
QY 153 ISTQGETSISNQPOQPTVLVTEDLLIEAPFGFEMRSDQSRYLEGPDNLRHVGVDPL 212  
Db 2375 VSWPGVFPTAGRRVPLPTV-----PW-----QQRQYWPDIPEDSRRHAAADPT 2417  
QY 213 HGADAALVAEELRLITEDPSLEEIPAGEW 242  
Db 2418 QGWFYRVDWPEIPRSLOKS---EEASRGSW 2444

## RESULT 12

US-09-568-480-5  
; Sequence 5, Application US/09568480  
; Patent No. 6355458  
; GENERAL INFORMATION:  
; APPLICANT: Schupp, Thomas  
; APPLICANT: Ligon, James  
; APPLICANT: Molnar, Istvan  
; APPLICANT: Zirkle, Ross

; APPLICANT: Cyr, Devon  
; APPLICANT: Goerlach, Joern  
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES  
; FILE REFERENCE: 4-30582A  
; CURRENT APPLICATION NUMBER: US/09/568,480  
; PRIOR FILING DATE: 2000-05-10  
; PRIOR FILING DATE: 1999-06-17  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 7257  
; TYPE: PRT  
; ORGANISM: Sorangium cellulosum  
US-09-568-480-5

Query Match 5.5%; Score 86.5; DB 3; Length 7257;  
Best Local Similarity 19.3%; Pred. No. 1.3e+02;  
Matches 52; Conservative 31; Mismatches 76; Indels 111; Gaps 11;  
QY 49 IAGENWPTVEIVDGTNDVNNALTSMFASKGVTCCGGVGE-----APPVAEEPPKI-- 99  
Db 2210 IAAVNGPE-QVVIAGVEQVQAIAAGFAARGARTKRLHVSHASHSPLEPMLEEFGRVAA 2268  
QY 100 ----KRPT-----SGK-----QVRQFYGIKPLH----- 118  
Db 2269 SVTYRRPSVLSNLGKVVADLSAPGYWYRVHREAVRFADGVKALHEAGAGTFFVEVGP 2328  
QY 119 -----LLVLSILVG-----SIAGIWIISGFTGPDVSRPVDKVAE 152  
Db 2329 KPTLLGLLPACLPAPAEPTLLASLRAGREAAAGVLEALGRLWAAG-----S 2374  
QY 153 ISTQGETSISNQPOQPTVLVTEDLLIEAPFGFEMRSDQSRYLEGPDNLRHVGVDPL 212  
Db 2375 VSWPGVFPTAGRRVPLPTV-----PW-----QQRQYWPDIPEDSRRHAAADPT 2417  
QY 213 HGADAALVAEELRLITEDPSLEEIPAGEW 242  
Db 2418 QGWFYRVDWPEIPRSLOKS---EEASRGSW 2444

## RESULT 13

US-09-568-486-5  
; Sequence 5, Application US/09568486  
; Patent No. 6355459  
; GENERAL INFORMATION:  
; APPLICANT: Schupp, Thomas  
; APPLICANT: Ligon, James  
; APPLICANT: Molnar, Istvan  
; APPLICANT: Zirkle, Ross  
; APPLICANT: Cyr, Devon  
; APPLICANT: Goerlach, Joern  
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES  
; FILE REFERENCE: 4-30582A  
; CURRENT APPLICATION NUMBER: US/09/568,486  
; PRIOR FILING DATE: 2000-05-10  
; PRIOR FILING DATE: 1999-06-17  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 7257  
; TYPE: PRT  
; ORGANISM: Sorangium cellulosum  
US-09-568-486-5

Query Match 5.5%; Score 86.5; DB 3; Length 7257;  
Best Local Similarity 19.3%; Pred. No. 1.3e+02;  
Matches 52; Conservative 31; Mismatches 76; Indels 111; Gaps 11;  
QY 49 IAGENWPTVEIVDGTNDVNNALTSMFASKGVTCCGGVGE-----APPVAEEPPKI-- 99  
Db 2210 IAAVNGPE-QVVIAGVEQVQAIAAGFAARGARTKRLHVSHASHSPLEPMLEEFGRVAA 2268

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QY 100 ----KRPT-----SGK-----QVROFYGIKPLH----- 118
Db 2269 SVTTRPSVLSVNLGKVADELSAPGYVVRHVREAVRFDAGVKALHEAGAGTFVEVGP 2328
QY 119 -----LLVLSILVG-----STAGIWIISGFTGPDVSRPVDKVAE 152
Db 2329 KPTLLGLLPACLPAPETLLASLRAGREAAAGVLEALGRLWAAG-----S 2374
QY 153 ISTOGETSISNQPOQPTVLVTEDLLIEAPFGFEMRSDEQSRYLEGPDPNLRHVGVDPL 212
Db 2375 VSWPGVFTAGRRVPLPTY-----PW-----QQRQYWPDIETPDSRRHAADPT 2417
QY 213 HGADAALVAEELRLITEDPSLEIPAGEW 242
Db 2418 QGWFRYVDWPEIPRSLOKS---EASRGSW 2444

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## RESULT 14

US-09-568-472-5

; Sequence 5, Application US/09568472

; Patent No. 6358719

; GENERAL INFORMATION:

; APPLICANT: Schupp, Thomas

; APPLICANT: Ligon, James

; APPLICANT: Molnar, Istvan

; APPLICANT: Zirkle, Ross

; APPLICANT: Cyr, Devon

; APPLICANT: Goerlach, Joern

; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

; FILE REFERENCE: 4-30582A

; CURRENT APPLICATION NUMBER: US/09/568,472

; CURRENT FILING DATE: 2000-05-10

; PRIOR APPLICATION NUMBER: 09/335,409

; PRIOR FILING DATE: 1999-06-17

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 7257

; TYPE: PRT

; ORGANISM: Sorangium cellulosum

US-09-568-472-5

Query Match 5.5%; Score 86.5; DB 3; Length 7257;

Best Local Similarity 19.3%; Pred. No. 1.3e+02;

Matches 52; Conservative 31; Mismatches 76; Indels 111; Gaps 11;

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QY 49 IAGENWPTVEIVDGTDNVVALTSMFASKGVTGCGGVGE-----APPVABEPPKI-- 99
Db 2210 IAAVNGPE-QVVIAGVEQVQAIAAGFAARGARTKRLHVSASHSPLMPEMLEEFGRVAA 2268

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QY 100 ----KRPT-----SGK-----QVROFYGIKPLH----- 118
Db 2269 SVTTRPSVLSVNLGKVADELSAPGYVVRHVREAVRFDAGVKALHEAGAGTFVEVGP 2328
QY 119 -----LLVLSILVG-----STAGIWIISGFTGPDVSRPVDKVAE 152
Db 2329 KPTLLGLLPACLPAPETLLASLRAGREAAAGVLEALGRLWAAG-----S 2374
QY 153 ISTOGETSISNQPOQPTVLVTEDLLIEAPFGFEMRSDEQSRYLEGPDPNLRHVGVDPL 212
Db 2375 VSWPGVFTAGRRVPLPTY-----PW-----QQRQYWPDIETPDSRRHAADPT 2417
QY 213 HGADAALVAEELRLITEDPSLEIPAGEW 242
Db 2418 QGWFRYVDWPEIPRSLOKS---EASRGSW 2444

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## RESULT 15

US-09-567-899-5

; Sequence 5, Application US/09567899

; Patent No. 6383787

; GENERAL INFORMATION:

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: December 3, 2004, 15:41:30 : Search time 150 Seconds  
(without alignments)  
713.246 Million cell updates/sec

Title: US-09-605-703B-2

Perfect score: 1566

Sequence: 1 MSTQTITITVLETATIDGP.....AETLVHKAQRNVIEHLTK 300

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
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- 9: /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep.\*
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- 11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*
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- 13: /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep.\*
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- 18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1566	100.0	300	9	US-09-738-626-4143
2	102	6.5	768	16	US-10-437-963-147646
3	101.5	6.5	391	16	US-10-437-963-161769
4	99	6.3	1325	15	US-10-282-122A-44953
5	98	6.3	350	9	US-09-732-618-6
6	97.5	6.2	554	15	US-10-282-122A-55617
7	96.5	6.2	554	15	US-10-282-122A-77990
8	96	6.1	444	17	US-10-425-115-192594
9	96	6.1	2734	14	US-10-359-012-12
10	96	6.1	3002	14	US-10-359-012-10
11	96	6.1	3002	14	US-10-359-012-20
12	96	6.1	4723	14	US-10-359-012-8
13	93.5	6.0	328	10	US-09-765-061B-76

14	93	5.9	211	15	US-10-425-114-57848	Sequence 57848, A
15	92.5	5.9	554	15	US-10-282-122A-56475	Sequence 56475, A
16	92.5	5.9	1012	15	US-10-282-122A-51060	Sequence 51060, A
17	91.5	5.8	524	14	US-10-369-493-12144	Sequence 12144, A
18	91	5.8	551	15	US-10-425-114-62590	Sequence 62590, A
19	90.5	5.8	413	15	US-10-282-122A-45260	Sequence 45260, A
20	90	5.7	214	16	US-10-437-963-138079	Sequence 138079, A
21	90	5.7	564	15	US-10-425-114-45446	Sequence 45446, A
22	90	5.7	594	14	US-10-259-165-334	Sequence 334, App
23	90	5.7	1291	17	US-10-425-115-274220	Sequence 274220, A
24	90	5.7	2551	15	US-09-808-880-3	Sequence 3, Appl
25	90	5.7	3816	10	US-09-808-880-3	Sequence 42026, A
26	89.5	5.7	334	16	US-10-767-701-42026	Sequence 47800, A
27	89	5.7	954	15	US-10-282-122A-47800	Sequence 27, Appl
28	89	5.7	1150	14	US-10-198-070-27	Sequence 200, App
29	89	5.7	1150	14	US-10-198-082-200	Sequence 1129, App
30	89	5.7	1150	16	US-10-408-785A-1129	Sequence 61385, A
31	88.5	5.7	330	15	US-10-282-122A-61385	Sequence 1693, App
32	88.5	5.7	369	15	US-10-389-566-1693	Sequence 13027, A
33	88.5	5.7	445	14	US-10-369-493-13027	Sequence 59433, A
34	88.5	5.7	554	15	US-10-282-122A-59433	Sequence 76817, A
35	88	5.6	448	15	US-10-282-122A-76817	Sequence 75726, A
36	88	5.6	554	15	US-10-282-122A-75726	Sequence 152007, A
37	88	5.6	1857	16	US-10-437-963-152007	Sequence 3504, App
38	88	5.6	2356	14	US-10-128-714-3504	Sequence 8504, App
39	88	5.6	3170	14	US-10-128-714-8504	Sequence 426, App
40	87.5	5.6	162	14	US-10-080-170-426	Sequence 426, App
41	87.5	5.6	162	16	US-10-080-170-426	Sequence 426, App
42	87.5	5.6	162	17	US-10-468-356-426	Sequence 426, App
43	87.5	5.6	163	9	US-09-996-634-130	Sequence 130, App
44	87.5	5.6	163	10	US-09-997-182-130	Sequence 130, App
45	87.5	5.6	163	10	US-09-997-181-130	Sequence 130, App

## ALIGNMENTS

### RESULT 1

US-09-738-626-4143  
; Sequence 4143, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIRO  
; APPLICANT: OCHIAI, KEIKO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TATEISHI, NAKO  
; APPLICANT: SENOH, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; APPLICANT: OZAKI, AKIO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738,626  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: JP 00/159162  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: JP 00/280988  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 7059  
; SOFTWARE: PatentIn ver. 3.0  
; SEQ ID NO 4143  
; LENGTH: 300  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-09-738-626-4143

Query Match 100.0%; Score 1566; DB 9; Length 300;  
Best Local Similarity 100.0%; Pred. No. 2e-147; Indels 0; Gaps 0;  
Matches 300; Conservative 0; Mismatches 0;

```

QY 1 MSTOTITITVLETATIDGPGETIYRYDLAAEGILDGWAHSAVLDDQVKQIAGENWPTVEIV 60
DB 1 MSTOTITITVLETATIDGPGETIYRYDLAAEGILDGWAHSAVLDDQVKQIAGENWPTVEIV 60

QY 61 VDGTDNVNALTSMFASKGVTCCGGVGEAPPVABEPPKIKRPTSGKQVRFYGIKPLHLL 120
DB 61 VDGTDNVNALTSMFASKGVTCCGGVGEAPPVABEPPKIKRPTSGKQVRFYGIKPLHLL 120

QY 121 LVSTLVSIGIWIISGFTGPDVSRPVDKVAEISTQGETSISNQPOQPTVLVTELLIE 180
DB 121 LVSTLVSIGIWIISGFTGPDVSRPVDKVAEISTQGETSISNQPOQPTVLVTELLIE 180

QY 181 APFGFVRSDQSRYLEGPDNLRHIVGVDPLHGADAAALVABEELRLITEDPSLEIPAG 240
DB 181 APFGFVRSDQSRYLEGPDNLRHIVGVDPLHGADAAALVABEELRLITEDPSLEIPAG 240

QY 241 EWGKTTIDYRETPGDGSHVLWTFWTDRLQNLVNGCHSKAAETLVHKAQCNVIEHLTK 300
DB 241 EWGKTTIDYRETPGDGSHVLWTFWTDRLQNLVNGCHSKAAETLVHKAQCNVIEHLTK 300

```

## RESULT 2

```

US-10-437-963-147646
; Sequence 147646, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 147646
; LENGTH: 768
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(768)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_48155C.1.pap
US-10-437-963-147646

```

```

Query Match 6.5%; Score 102; DB 16; Length 768;
Best Local Similarity 23.5%; Pred. No. 1;
Matches 58; Conservative 28; Mismatches 83; Indels 78; Gaps 11;

QY 43 LDQ-VKQIAGENWPTVEIVDG-----TDNVNALTSMFASKGVTCCGGVGEAPPVABE 94
DB 153 IDQIVDSIAGEN---VGVYVDLVVTRHQDTLLQDLAETFDLSRSTCMKLNPE----- 203

QY 95 EPPKIKRPTSGKQVRYGKPKPLHLLVLSIGIWIISGFTGPDVSRPVDKVAEIS 154
DB 204 -----KCVFGVPAGKLLRVHGMHGRPEINIEAGKEGVAPIQAPQTLWAVC 249

QY 155 TQGETSISNQPOQPQ-----PVLVTELLIEAPFGFVRSDQSRYLEGPDNLRHIVGVD 210
DB 250 MVGSGASSQPAESLPLPILV-----AP-----GPEEPILLIYAT 287

QY 211 PLHGADAAALVAE-----ELRR-----LITEDPS-----LEIPAGEWKEKTTIDY 250
DB 288 P-HSVSAALVVERDEGLRREPVGKPGVGLTSDGSPSPNSPMPAPNPREGPEVFGVE 346

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QY 251 RETPGDG 257
DB 347 REAPADG 353

```

## RESULT 3

```

US-10-437-963-161769
; Sequence 161769, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 161769
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_60923C.1.pap
US-10-437-963-161769

```

Query Match 6.5%; Score 101.5; DB 16; Length 391;

Best Local Similarity 24.4%; Pred. No. 0.43; Matches 52; Conservative 32; Mismatches 68; Indels 61; Gaps 13;

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QY 14 ATIFDGPBT-IYRYDLAAEGILDGWAH-----SAVLDDQVKQIAGENWPTVEIVVDGTDN 66
DB 190 ATLFWAPITNSERY---EGSVDFWSDVYGINMSALVPLAKKFTSE-PSIEII--GGEN 242

QY 67 VVNALTSMFASKGVTCCGGVGEAPPVABEPPKIKRPTSGKQVRFYGIKPLHLLVLSILV 126
DB 243 V---LSWPFVVKHIDCYTFKAE-----ELKSFTTKYKVSMM-LAPIHG----- 283

QY 127 GSIAGIWIISGFTG-----PVDSRPVDKVAEISTQGETS-----ISNQPOQPQPT----- 170
DB 284 ---GLWEFEVFNGPSNPTDKSPDLNPLDVIRKRRRSGSDPVLVSTAPDEBPTHWHT 339

QY 171 -----VLVTELLIEAPFGFVRSDQSRYL 196
DB 340 ILYFPDPIEVKQDQIIIEGSKVS-QSEENPRFL 371

```

## RESULT 4

```

US-10-282-122A-44953
; Sequence 44953, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Chlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A

```

;; CURRENT FILING DATE: 2003-02-20  
;; PRIOR APPLICATION NUMBER: 60/191,078  
;; FILING DATE: 2000-03-21  
;; PRIOR APPLICATION NUMBER: 60/206,848  
;; FILING DATE: 2000-05-23  
;; PRIOR APPLICATION NUMBER: 60/207,727  
;; FILING DATE: 2000-05-26  
;; PRIOR APPLICATION NUMBER: 60/230,335  
;; FILING DATE: 2000-09-06  
;; PRIOR APPLICATION NUMBER: 60/230,347  
;; FILING DATE: 2000-09-09  
;; PRIOR APPLICATION NUMBER: 60/242,578  
;; FILING DATE: 2000-10-23  
;; PRIOR APPLICATION NUMBER: 60/253,625  
;; FILING DATE: 2000-11-27  
;; PRIOR APPLICATION NUMBER: 60/257,931  
;; FILING DATE: 2000-12-22  
;; PRIOR APPLICATION NUMBER: 60/267,636  
;; FILING DATE: 2001-02-09  
;; PRIOR APPLICATION NUMBER: 60/269,308  
;; FILING DATE: 2001-02-16  
;; Remaining Prior Application data removed - See File Wrapper or PALM.  
;; NUMBER OF SEQ ID NOS: 78614  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 44953  
;; LENGTH: 1325  
;; TYPE: PRT  
;; ORGANISM: Acinetobacter baumannii  
;; FEATURE:  
;; NAME/KEY: MISC FEATURE  
;; LOCATION: (479)..(479)  
;; OTHER INFORMATION: X=any amino acid  
;; FEATURE:  
;; NAME/KEY: MISC FEATURE  
;; LOCATION: (726)..(726)  
;; OTHER INFORMATION: X=any amino acid  
;; FEATURE:  
;; NAME/KEY: MISC FEATURE  
;; LOCATION: (751)..(751)  
;; OTHER INFORMATION: X=any amino acid  
;; FEATURE:  
;; NAME/KEY: MISC FEATURE  
;; LOCATION: (762)..(762)  
;; OTHER INFORMATION: X=any amino acid  
;; FEATURE:  
;; NAME/KEY: MISC FEATURE  
;; LOCATION: (779)..(779)  
;; OTHER INFORMATION: X=any amino acid  
;; FEATURE:  
;; NAME/KEY: MISC FEATURE  
;; LOCATION: (799)..(799)  
;; OTHER INFORMATION: X=any amino acid  
US-10-282-122A-44953

Query Match 6.3%; Score 99; DB 15; Length 1325;  
Best Local Similarity 22.8%; Pred. No. 4.6;  
Matches 84; Conservative 27; Mismatches 125; Indels 132; Gaps 18;  
QY 2 STQRTITVLTATIEDPQETIYVDLAAEGILDGWAHSAVLDOVKQIA-----50  
Db 116 STVTVYNGDTAVVAGPDG--SWSVPNGDNG-----DEVAIATDPAGNPSLPG 166  
QY 51 -----GENPFTVEIVDG--TDNVNVALTSMFASKGVTGCGVGEAPPVVAEPPKIKR 101  
Db 167 TAIVDAVGPNTDGNNFTVDSVTADNVINASE---ASGNVTVTGLKNVPADAAN-----217  
QY 102 PISGKQVRFQVIGIKPLHLLVLSIL-----VGSSTAGIWI---SGFTGPVDSRPVD 148  
Db 218 -----TTVTVINGQTYTATVDSAGTWTVSVPGLVADTKTIDA 259  
QY 149 KVAEISTQGETSISNQPOPTVLVTEDLLIEAPFG-----FEMRSDEQSRYLEG-- 198  
Db 260 KVTFTDAAGNSSVNDTQTYTVDITAPDAPVINFVNGTDPTGTAEPSITVTIYPDGTT 319

QY 199 -----PDFNLRIH-----VGWDP-----LHG-----ADAALVAEELRLIT 229  
Db 320 ATVVAGTGDGWSVNEPGLVDGDTVTATATDPAAGTSLPGTGTVSADITAPVVALDDVLT 379  
QY 230 ED--PSLE-----EIPAGEWGEKT--TIDYRETP--GDGSHVLWVTWFD 267  
Db 380 NDSTPALCTGVNDPTATVVVNVVDGVDYPAVNNNGDGTWLADNTLPTLADGPHITVT--A 437  
QY 268 TDRQLNVG 275  
Db 438 TDAAGNVG 445  
RESULT 5  
US-09-732-618-6  
;; Sequence 6, Application US/09732618  
;; Patent No. US20010044939A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Abell, Lynn  
;; APPLICANT: Falco, Carl  
;; APPLICANT: Farnu, Omolayo O.  
;; TITLE OF INVENTION: Small Subunit of Plant Acetolactate Synthase  
;; FILE REFERENCE: BB1435 US NA  
;; CURRENT APPLICATION NUMBER: US/09/732,618  
;; CURRENT FILING DATE: 2000-12-08  
;; PRIOR APPLICATION NUMBER: 60/174,437  
;; PRIOR FILING DATE: 2000-01-04  
;; NUMBER OF SEQ ID NOS: 43  
;; SOFTWARE: Microsoft Office 97  
;; SEQ ID NO 6  
;; LENGTH: 350  
;; TYPE: PRT  
;; ORGANISM: Zea mays  
US-09-732-618-6

Query Match 6.3%; Score 98; DB 9; Length 350;  
Best Local Similarity 24.2%; Pred. No. 0.83;  
Matches 52; Conservative 29; Mismatches 68; Indels 66; Gaps 10;  
QY 26 YDLAEGILDGWAHSAVLDOVKQIAGENWPTVEIIVVDGTDNVNVALTSMFASKGVTGCGV 85  
Db 155 YESSANQVLD--AHMGVLD--DDATGLCSHTLSILVNDGPGVNLIVTGVFARRGYNIOQL 211  
QY 86 GVEAPPVABEPPKIKPTS-----GKVRQFVGIKPLH-----LLLV 122  
Db 212 AVG-----SAKEGISHITTVFGTVESIGKLVQQLYKLIDVHEVDITHSPFAERELMLI 267  
QY 123 SILVGSIAGIWVISGFTGPVDSRPVDKVAEISTQGETSISNQPOPTVLVTEDL-----177  
Db 268 KVSNTAA-----RREILDIAEIPRAKPIDVSDH---TVTLQLTGDLDKMVA 311  
QY 178 ---LIEAPEG-----FEMRSDEQSRYLEG 198  
Db 312 LORLLE-PYGICEVARTGRVALVRSEKVDKYLRG 345

US-10-282-122A-55617  
;; Sequence 55617, Application US/10282122A  
;; Publication No. US20040029129A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wang, Liangsu  
;; APPLICANT: Zamudio, Carlos  
;; APPLICANT: Malone, Cheryl  
;; APPLICANT: Haselbeck, Robert  
;; APPLICANT: Ohlsen, Kari  
;; APPLICANT: Zyskind, Judith  
;; APPLICANT: Wall, Daniel  
;; APPLICANT: Trawick, John  
;; APPLICANT: Carr, Grant  
;; APPLICANT: Yamamoto, Robert  
;; APPLICANT: Forsyth, R.

```

; APPLICANT: XU, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55617
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Enterobacter cloacae
US-10-282-122A-55617

Query Match      6.2%; Score 97.5; DB 15; Length 554;
Best Local Similarity 23.5%; Pred. No. 1.8;
Matches 56; Conservative 33; Mismatches 92; Indels 57; Gaps 13;

Qy 71 LTMFASKGVTGGV-GVEAPPVABEPKIKRTSGKVRQFYGIKPLHLLVSLVGS 129
Db 24 LSLMRHRGPDMSGVASDKAILAHERLSIVDNAGAQ--PLYNEKKTALAVN--GSI 78

Qy 130 AGIWIISGFTGPDVSRPDKVA-EISTQGETSISNQPOPTVLTEDLLIEAPGFM 188
Db 79 YNHOALRAEYV-----DRIYATQSGDCEVILALYQKGFEPF--DDU--QGMFAFY 127

Qy 189 SDEQSYLEGDPNLRHVGVDEL-----HGADAALVAEELRLITEDPSLEEIPAG 242
Db 128 DSEKDAYLIGRD-----HIGIIPLYMGHYEHG--NFYVASEMKALVPVCRTIKEP 180

Qy 243 -----GKTTIDYRETGDSHVLWVTFDTRQLNVGCHSKAAETLVHKAQCENV 295
Db 181 LWSKDGSIYSYQRD-----WFDYD-----PVKDNVTDKAEILRQALE 217

RESULT 7
US-10-282-122A-77990
; Sequence 77990, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haeelbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: XU, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

```

```

; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77990
; LENGTH: 554
; TYPE: PRT
; ORGANISM: Yersinia pestis
US-10-282-122A-77990

Query Match      6.2%; Score 96.5; DB 15; Length 554;
Best Local Similarity 27.0%; Pred. No. 2.3;
Matches 34; Conservative 19; Mismatches 38; Indels 35; Gaps 7;

Qy 179 IEAPGFMRSDEOSRYLEGDPNLRHVGVDPILH-GADA---ALVAEELRLITEDPS 234
Db 118 LQGMFAFVLYDTEKDAYLIGRD-----HLGIIPLYMGHDEHGNMFVASEMKALVP 172

Qy 235 EEIPAGW-----GKTTIDYRETGDSHVLWVTFDTRQLNVGCHSKAAETLVHKA 289
Db 173 KEFPAGSYLWSQDGEIREYVHRD-----WFDYD-----HVK--DNVTDKI 211

Qy 290 CENVIE 295
Db 212 LANALE 217

RESULT 8
US-10-425-115-192594
; Sequence 192594, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 192594
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(444)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:

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OTHER INFORMATION: Clone ID: MRT4577\_10722C.1.pep  
US-10-423-115-192594

Query Match 6.1%; Score 96; DB 17; Length 444;  
Best Local Similarity 23.7%; Pred. No. 1.9;  
Matches 51; Conservative 30; Mismatches 68; Indels 66; Gaps 10;  
QY 26 YDLAEGILDGWAHSAVLDDQVKTQAGENWPTVEIIVDGTNDVVALTSMFASKGVTGCGV 85  
DB 249 YESSANQLVD--AHWGVLDD--DDATGLCSHTLSILVNDPCGVLNIVTGVFAARGYNTQSL 305  
QY 86 GVEAPPVAAEPPKIKRPTS-----GKQVRFYGIKPLH-----LLLV 122  
DB 306 AVG-----SAEKREGISRIITVVPGTVESIGKLVQQLYKLLDVHEVDIITHSPFAERLMLI 361  
QY 123 SILVSGIAGIWIISFTGPDVSRPVDKVAEISTQGETSISNQPOPOPTVLVTEDL----- 177  
DB 362 KVSNTAA-----RKEILDIAEIFRAKPDVSDH-----TVTLQLTGDLDKMVA 405  
QY 178 ---LIEAPFG-----FEMRSDEQSRYLEG 198  
DB 406 LQRLLE-PYGICEVARTGEVALVRESKYDLRG 439

## RESULT 9

US-10-359-012-12  
; Sequence 12, Application US/10359012  
; Publication No. US20030232419A1  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: KOLODKIN, Alex L.  
; APPLICANT: TERMAN, Jon R.  
; APPLICANT: MAO, Tianyi  
; APPLICANT: PASTERKAMP, Ronald J.  
; APPLICANT: YU, Hung-Hsiang  
; TITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPT  
; TITLE OF INVENTION: AND METHODS OF USING THE SAME  
; FILE REFERENCE: JHU1840-3  
; CURRENT APPLICATION NUMBER: US/10/359,012  
; PRIOR FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: US 60/388,325  
; PRIOR FILING DATE: 2002-06-13  
; PRIOR APPLICATION NUMBER: US 60/384,302  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: US 60/354,178  
; PRIOR FILING DATE: 2002-02-04  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 12  
; LENGTH: 2734  
; TYPE: PRT  
; ORGANISM: Drosophila  
US-10-359-012-12

Query Match 6.1%; Score 96; DB 14; Length 2734;  
Best Local Similarity 20.6%; Pred. No. 26;  
Matches 57; Conservative 36; Mismatches 92; Indels 92; Gaps 11;  
QY 40 SAVLDQVKQIAGENWPTVEIIVDGTNDVVALTSMFASKGVTGCGVGEAPPVAAEPPKI 99  
DB 1892 SMISQTQPTTTERSEALTVTSPDTSPPVLDQFAS--MLAAGKGDSTPSSEQQPKT 1949  
QY 100 KRPTSGKQVRFYGIKPLHLLVLSILVSGIAGIWIISFTGPDVSRPVDKVAEISTQGET 159  
DB 1950 STVTSSS-----TGP-----NSSTTG-- 1965  
QY 160 SISNQPOPTVLVTEDLIEAPF--GFEMR-----SDEQSRYLEGPDNLRHVGV--- 209  
DB 1966 NVSKEPQ-----EEDLQIOFEYVRLAQORISQISQTRKSKSGEAPNLQNSAPVIE 2018  
QY 210 ---DPLHGAADALVAEELR-----RLITEDPSLEEIPAGEWGEKTTIDYRETGCG 257  
DB 2019 SAEDPAKPAEELVSNRPTT--SISGKVPETLSSKLEITKERTKQKDLI----- 2069

QY 258 SHVLVWTWFTDRLQNVGCHSKAAETLVHKAQCRNVI 294  
DB 2070 -HDLVMDKLQSKKQLN-----AEKRLHRSQRSL 2098

## RESULT 10

US-10-359-012-10  
; Sequence 10, Application US/10359012  
; Publication No. US20030232419A1  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: KOLODKIN, Alex L.  
; APPLICANT: TERMAN, Jon R.  
; APPLICANT: MAO, Tianyi  
; APPLICANT: PASTERKAMP, Ronald J.  
; APPLICANT: YU, Hung-Hsiang  
; TITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPT  
; TITLE OF INVENTION: AND METHODS OF USING THE SAME  
; FILE REFERENCE: JHU1840-3  
; CURRENT APPLICATION NUMBER: US/10/359,012  
; CURRENT FILING DATE: 2003-02-04  
; PRIOR APPLICATION NUMBER: US 60/388,325  
; PRIOR FILING DATE: 2002-06-13  
; PRIOR APPLICATION NUMBER: US 60/384,302  
; PRIOR FILING DATE: 2002-05-30  
; PRIOR APPLICATION NUMBER: US 60/354,178  
; PRIOR FILING DATE: 2002-02-04  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 10  
; LENGTH: 3002  
; TYPE: PRT  
; ORGANISM: Drosophila  
US-10-359-012-10

Query Match 6.1%; Score 96; DB 14; Length 3002;  
Best Local Similarity 20.6%; Pred. No. 30;  
Matches 57; Conservative 36; Mismatches 92; Indels 92; Gaps 11;  
QY 40 SAVLDQVKQIAGENWPTVEIIVDGTNDVVALTSMFASKGVTGCGVGEAPPVAAEPPKI 99  
DB 2160 SMISQTQPTTTERSEALTVTSPDTSPPVLDQFAS--MLAAGKGDSTPSSEQQPKT 2217  
QY 100 KRPTSGKQVRFYGIKPLHLLVLSILVSGIAGIWIISFTGPDVSRPVDKVAEISTQGET 159  
DB 2218 STVTSSS-----TGP-----NSSTTG-- 2233  
QY 160 SISNQPOPTVLVTEDLIEAPF--GFEMR-----SDEQSRYLEGPDNLRHVGV--- 209  
DB 2234 NVSKEPQ-----EEDLQIOFEYVRLAQORISQISQTRKSKSGEAPNLQNSAPVIE 2286  
QY 210 ---DPLHGAADALVAEELR-----RLITEDPSLEEIPAGEWGEKTTIDYRETGCG 257  
DB 2287 SAEDPAKPAEELVSNRPTT--SISGKVPETLSSKLEITKERTKQKDLI----- 2337  
QY 258 SHVLVWTWFTDRLQNVGCHSKAAETLVHKAQCRNVI 294  
DB 2338 -HDLVMDKLQSKKQLN-----AEKRLHRSQRSL 2366

## RESULT 11

US-10-359-012-20  
; Sequence 20, Application US/10359012  
; Publication No. US20030232419A1  
; GENERAL INFORMATION:  
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
; APPLICANT: KOLODKIN, Alex L.  
; APPLICANT: TERMAN, Jon R.  
; APPLICANT: MAO, Tianyi  
; APPLICANT: PASTERKAMP, Ronald J.  
; APPLICANT: YU, Hung-Hsiang  
; TITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPT

```
; TITLE OF INVENTION: AND METHODS OF USING THE SAME
; FILE REFERENCE: JHU1840-3
; CURRENT APPLICATION NUMBER: US/10/359,012
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/389,325
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 60/384,302
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 60/354,178
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 3002
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Drosophila G-W mutant. G residues 134, 136, 139 of Drosophila M1
; OTHER INFORMATION: CAL changed to W residues
US-10-359-012-20

Query Match 6.1%; Score 96; DB 14; Length 3002;
Best Local Similarity 20.6%; Pred. No. 30;
Matches 57; Conservative 36; Mismatches 92; Indels 92; Gaps 11;

QY 40 SAVLDQVKQIAGENWPTVEIVDGTDNVVALTSMFASKGVTGGVGVAEAPPVVAEPPKI 99
DB 2160 SMIISQTPPTTESEALTVVTSPDLTSSSPRLVDQFAS--MLAAGKGDSTPSSSEQPKT 2217
QY 100 KRPTSGKQVQFYGIKPLHLLVLSILVGSIAGIWISGFTGPVDSRPVVKVAEISTQGET 159
DB 2218 STVTSSS-----TGP-----NSSTTG-- 2233
QY 160 SISNQPPQPTVLVTEDLLIEAPF--GFEMR-----SDEQSYLEGPDNLRHVG-- 209
DB 2234 NVSKEPQ-----EEDLIQIQFVRLAQQRISQISTQRRKSKGEAPNLQLNSAPVIE 2286
QY 210 ---DELHGADAALVAEELR-----RLITDPSLEEIPAGEWGEKTTIDYRETFGDG 257
DB 2287 SAEDPAKPAEPLVSMRPTTSISGKVPETLSSKLEETKERTKQKDLI----- 2337
QY 258 SHVLWVTWFTDRLQNVGCHSKAAETLVHKAQCRNVI 294
DB 2338 -HDLVMDKLQSKQLN-----AEKLRHSRQSRLL 2366

RESULT 12
US-10-359-012-8
; Sequence 8, Application US/10359012
; Publication No. US20030232419A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: KOLODKIN, Alex L.
; APPLICANT: THERMAN, Jon R.
; APPLICANT: MAO, Tianyi
; APPLICANT: PASTERKAMP, Ronald J.
; APPLICANT: YU, Hung-Hsiang
; TITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPT
; FILE REFERENCE: JHU1840-3
; CURRENT APPLICATION NUMBER: US/10/359,012
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/389,325
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 60/384,302
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 60/354,178
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 4723
; TYPE: PRT

; TITLE OF INVENTION: AND METHODS OF USING THE SAME
; FILE REFERENCE: JHU1840-3
; CURRENT APPLICATION NUMBER: US/10/359,012
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/389,325
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 60/384,302
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 3002
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Drosophila G-W mutant. G residues 134, 136, 139 of Drosophila M1
; OTHER INFORMATION: CAL changed to W residues
US-10-359-012-20

Query Match 6.1%; Score 96; DB 14; Length 3002;
Best Local Similarity 20.6%; Pred. No. 30;
Matches 57; Conservative 36; Mismatches 92; Indels 92; Gaps 11;

QY 40 SAVLDQVKQIAGENWPTVEIVDGTDNVVALTSMFASKGVTGGVGVAEAPPVVAEPPKI 99
DB 2160 SMIISQTPPTTESEALTVVTSPDLTSSSPRLVDQFAS--MLAAGKGDSTPSSSEQPKT 2217
QY 100 KRPTSGKQVQFYGIKPLHLLVLSILVGSIAGIWISGFTGPVDSRPVVKVAEISTQGET 159
DB 2218 STVTSSS-----TGP-----NSSTTG-- 2233
QY 160 SISNQPPQPTVLVTEDLLIEAPF--GFEMR-----SDEQSYLEGPDNLRHVG-- 209
DB 2234 NVSKEPQ-----EEDLIQIQFVRLAQQRISQISTQRRKSKGEAPNLQLNSAPVIE 2286
QY 210 ---DELHGADAALVAEELR-----RLITDPSLEEIPAGEWGEKTTIDYRETFGDG 257
DB 2287 SAEDPAKPAEPLVSMRPTTSISGKVPETLSSKLEETKERTKQKDLI----- 2337
QY 258 SHVLWVTWFTDRLQNVGCHSKAAETLVHKAQCRNVI 294
DB 2338 -HDLVMDKLQSKQLN-----AEKLRHSRQSRLL 2366

RESULT 12
US-10-359-012-8
; Sequence 8, Application US/10359012
; Publication No. US20030232419A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: KOLODKIN, Alex L.
; APPLICANT: THERMAN, Jon R.
; APPLICANT: MAO, Tianyi
; APPLICANT: PASTERKAMP, Ronald J.
; APPLICANT: YU, Hung-Hsiang
; TITLE OF INVENTION: MOLECULES INTERACTING WITH CASL (MICAL) POLYNUCLEOTIDES, POLYPEPT
; FILE REFERENCE: JHU1840-3
; CURRENT APPLICATION NUMBER: US/10/359,012
; CURRENT FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/389,325
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 60/384,302
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 60/354,178
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 4723
; TYPE: PRT

; ORGANISM: Drosophila
US-10-359-012-8

Query Match 6.1%; Score 96; DB 14; Length 4723;
Best Local Similarity 20.6%; Pred. No. 58;
Matches 57; Conservative 36; Mismatches 92; Indels 92; Gaps 11;

QY 40 SAVLDQVKQIAGENWPTVEIVDGTDNVVALTSMFASKGVTGGVGVAEAPPVVAEPPKI 99
DB 3881 SMIISQTPPTTESEALTVVTSPDLTSSSPRLVDQFAS--MLAAGKGDSTPSSSEQPKT 3938
QY 100 KRPTSGKQVQFYGIKPLHLLVLSILVGSIAGIWISGFTGPVDSRPVVKVAEISTQGET 159
DB 3939 STVTSSS-----TGP-----NSSTTG-- 3954
QY 160 SISNQPPQPTVLVTEDLLIEAPF--GFEMR-----SDEQSYLEGPDNLRHVG-- 209
DB 3955 NVSKEPQ-----EEDLIQIQFVRLAQQRISQISTQRRKSKGEAPNLQLNSAPVIE 4007
QY 210 ---DELHGADAALVAEELR-----RLITDPSLEEIPAGEWGEKTTIDYRETFGDG 257
DB 4008 SAEDPAKPAEPLVSMRPTTSISGKVPETLSSKLEETKERTKQKDLI----- 4058
QY 258 SHVLWVTWFTDRLQNVGCHSKAAETLVHKAQCRNVI 294
DB 4059 -HDLVMDKLQSKQLN-----AEKLRHSRQSRLL 4087

RESULT 13
US-09-765-061B-76
; Sequence 76, Application US/09765061B
; Publication No. US20030022165A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Texas System
; TITLE OF INVENTION: Mutations in a No. US20030022165A1el Photoreceptor-pineal gene 17:
; FILE REFERENCE: 96606/16UTL
; CURRENT APPLICATION NUMBER: US/09/765,061B
; CURRENT FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(328)
; OTHER INFORMATION: Mouse AIPL1 Protein
US-09-765-061B-76

Query Match 6.0%; Score 93.5; DB 10; Length 328;
Best Local Similarity 20.8%; Pred. No. 2.1;
Matches 59; Conservative 42; Mismatches 91; Indels 91; Gaps 12;

QY 59 IWDGTDNVVALTIS---MEASKGVTGGVGVAEAPPVVAEPPKIKRPTSGKQVQFYGIK 115
DB 16 ILHGTGELPNFTGSRVTFHRTMKD-----EERTVIDSKQVQPMNS-IIGNMPKLE 70
QY 116 PLHLLVLSILVGSIAGIWISGFTG--FVDSRPVVKVAE-----ISTQG----- 157
DB 71 VWEITLTSRVLGEVAEFPWCDDTIHTGVYPMLSRSLRQVAEGKDPTSWHVHTCGLANMFAYH 130
QY 158 ---ETSISNQPPQPTVLVTEDLLIEAPGFE-----MRSDEQSYLEGPDNLRHVG 208
DB 131 TLGYEDDLDELQEPQLPFLYFLLQVEAPNEYQRETNWLNNEERMQ-----A 177
QY 209 VDPLHGA-----DAALVAEE---LRLITDPSLEEIPAGEWGEKTTIDYRET 253
DB 178 VPLLHGEGRNLYKLGRYDQATKYQEAIVCLRNLTQKEPWE----- 219
QY 254 PGDGSVLWVTWFTDRLQNVGCHSKAAETLVHKAQCRNVI 296
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Db 220 -----VEWLKLERMINT-LILNYCQCLLKKEEYEVLEH 252

RESULT 14

US-10-425-114-57848

; Sequence 57848, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 57848

; LENGTH: 211

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: UC-ZMFLB73253G07\_FLI.pep

US-10-425-114-57848

Query Match 5.9%; Score 93; DB 15; Length 211;

Best Local Similarity 24.0%; Pred. No. 1.2;

Matches 44; Conservative 26; Mismatches 73; Indels 40; Gaps 7;

Qy 61 VDGTDNVNALTSMFASKGV---TCGGV-----GVEAP--PVAEEPPKIKRP 102

Db 42 VGGYDRLVDLLINRQAKCVLRSTLSGLYSTLDGRISGGQGLSPRPVPSVAVPER 101

Qy 103 TSGKQVRFYGIKPLHLILLVLSIAGIIVISGFTGPVDSRPVDKVAEISTQGETSIS 162

Db 102 VHPK-----SLLAFVPGFAVVAIGEAVDAKFDLVPKVLARIPITVS 145

Qy 163 NQOPQPTVLTEDLL-IEAPFGFEMRSDQSRVLEGPDPNLRHVGVDPHLHGADALVA 221

Db 146 EMVAPDAVLDAALELPDVGAPVAGLRADAVA-LAAGP---LARVAVAEAVDAVAVA 200

Qy 222 EEL 224

Db 201 EAL 203

RESULT 15

US-10-282-122A-56475

; Sequence 56475, Application US/10282122A

; Publication No. US20040029129A1

; GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos

; APPLICANT: Malone, Cheryl

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari

; APPLICANT: Zyskind, Judith

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John

; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert

; APPLICANT: Forsyth, R.

; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

; FILE REFERENCE: ELTRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 56475

; LENGTH: 554

; TYPE: PRT

; ORGANISM: Escherichia coli

US-10-282-122A-56475

Query Match 5.9%; Score 92.5; DB 15; Length 554;

Best Local Similarity 24.6%; Pred. No. 5.7;

Matches 31; Conservative 21; Mismatches 39; Indels 35; Gaps 6;

Qy 179 IEAPFGFEMRSDQSRVLEGPDPNLRHVGVDPHLH-GAD---AALVAEELRLITEDPSL 234

Db 118 LQGMFAFALYDSEKDAYLLIGRD-----HLGIPLMYGYDEHGQLYVASEMKALVPVCRTI 172

Qy 235 EETPAGEW-----GEKTTIDYRETGDSGHVLTWTFDTRDNLNVGCHSKAAETLVHKAQ 289

Db 173 KEFPAGSYLWSQDGEIRSYHHRD-----WFDYD-----AVKDNVTDKNE 211

Qy 290 CRNVIE 295

Db 212 LROALE 217

Search completed: December 3, 2004, 15:55:25

Job time : 151 secs

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